

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 21, 2001, 14:14:51 ; Search time 36.86 Seconds
(without alignments)
213.833 Million cell updates/sec

Title: US-09-202-035-1
Perfect score: 288
Sequence: 1 KORQKPPSKPNDPHEVFP.....NNPTCWAICKRIPNKKPGKK 49

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1009251 seqs, 160854530 residues

Total number of hits satisfying chosen parameters: 1009251

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: /cgn2_6/ptodata/2/paa/PCRUS_COMB.pep.*
 - 2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
 - 3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
 - 4: /cgn2_6/ptodata/2/paa/US08_COMB.pep.*
 - 5: /cgn2_6/ptodata/2/paa/US09_COMB.pep.*
 - 6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*
 - 7: /cgn2_6/ptodata/2/paa/US083_COMB.pep.*
 - 8: /cgn2_6/ptodata/2/paa/US084_COMB.pep.*
 - 9: /cgn2_6/ptodata/2/paa/US085_COMB.pep.*
 - 10: /cgn2_6/ptodata/2/paa/US086_COMB.pep.*
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 - 21: /cgn2_6/ptodata/2/paa/US097_COMB.pep.*
 - 22: /cgn2_6/ptodata/2/paa/US098_COMB.pep.*
 - 23: /cgn2_6/ptodata/2/paa/US099_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	288	100.0	49	16	US-09-202-035-1
2	288	100.0	49	16	US-09-202-035-32
3	288	100.0	49	16	US-09-202-035-36
4	288	100.0	49	16	US-09-202-035-40
5	288	100.0	49	16	US-09-202-035-42
6	288	100.0	49	16	US-09-202-035-43
7	288	100.0	298	23	US-60-208-701-2
8	285	99.0	49	16	US-09-202-035-2
9	285	99.0	49	16	US-09-202-035-3
10	285	99.0	49	16	US-09-202-035-5

11	285	99.0	49	16	US-09-202-035-6	Sequence 6, Appl
12	285	99.0	49	16	US-09-202-035-7	Sequence 7, Appl
13	285	99.0	49	16	US-09-202-035-8	Sequence 8, Appl
14	285	99.0	232	12	US-08-896-442-4	Sequence 4, Appl
15	285	99.0	232	16	US-09-272-262-4	Sequence 4, Appl
16	285	99.0	298	4	US-08-001-534-8	Sequence 8, Appl
17	285	99.0	298	4	US-08-001-534A-8	Sequence 8, Appl
18	285	99.0	298	7	US-08-344-639-8	Sequence 8, Appl
19	285	99.0	298	7	US-08-344-639C-8	Sequence 8, Appl
20	285	99.0	298	7	US-08-344-639D-8	Sequence 8, Appl
21	285	99.0	298	7	US-08-344-639D-8	Sequence 8, Appl
22	285	99.0	298	8	US-08-467-961-8	Sequence 8, Appl
23	285	99.0	298	8	US-08-467-963-8	Sequence 8, Appl
24	285	99.0	298	8	US-08-467-963B-8	Sequence 8, Appl
25	285	99.0	298	8	US-08-467-969-8	Sequence 8, Appl
26	285	99.0	298	12	US-08-834-204-8	Sequence 8, Appl
27	285	99.0	298	12	US-08-838-189-8	Sequence 8, Appl
28	285	99.0	298	12	US-08-838-189A-8	Sequence 8, Appl
29	285	99.0	298	12	US-08-838-189B-8	Sequence 8, Appl
30	285	99.0	298	12	US-08-838-189C-8	Sequence 8, Appl
31	285	99.0	298	12	US-08-838-189D-8	Sequence 8, Appl
32	285	99.0	298	12	US-08-852-344-8	Sequence 8, Appl
33	285	99.0	298	12	US-08-852-344A-8	Sequence 8, Appl
34	285	99.0	298	12	US-08-852-344B-8	Sequence 8, Appl
35	285	99.0	298	12	US-08-852-344C-8	Sequence 8, Appl
36	285	99.0	298	12	US-08-852-344D-8	Sequence 8, Appl
37	285	99.0	298	16	US-09-272-262-2	Sequence 2, Appl
38	285	99.0	298	16	US-09-272-262-2	Sequence 2, Appl
39	283	98.3	49	16	US-09-479-240-8	Sequence 8, Appl
40	270	93.8	101	18	US-09-462	Sequence 16, Appl
41	267	92.7	101	18	US-09-462	Sequence 15, Appl
42	263	91.3	49	16	US-09-202-035-18	Sequence 18, Appl
43	261	90.6	49	16	US-09-202-035-17	Sequence 17, Appl
44	252	87.5	101	18	US-09-462	Sequence 17, Appl
45	249	86.5	42	16	US-09-202-035-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1
US-09-202-035-1
; Sequence 1, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; TITLE OF INVENTION: Respiratory Syncytial Virus
; FILE REFERENCE: 41585200100
; CURRENT APPLICATION NUMBER: US/09/202,035
; CURRENT FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; EARLIER FILING DATE: 1996-06-05
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 49
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-09-202-035-1

Query Match 100.0%; Score 288; DB 16; Length 49;
Best Local Similarity 100.0%; Pred. No. 5.8e-27;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KORQKPPSKPNDPHEVFPVPCISCSNNPTCWAICKRIPNKKPGKK 49
DB 1 KORQKPPSKPNDPHEVFPVPCISCSNNPTCWAICKRIPNKKPGKK 49
RESULT 2

[illegible]

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Query Match      100.0%; Score 288; DB 23; Length 298;
Best Local Similarity 100.0%; Pred. No. 3,7e-26;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSPKPNDFHEFEVNFVPCISCSNNPTCWAICKRIPNKKPKKK 49
Db 149 KORQKPPSPKPNDFHEFEVNFVPCISCSNNPTCWAICKRIPNKKPKKK 197

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RESULT 10
US-09-202-035-5
; Sequence 5, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of Respiratory Syncytial Virus
; TITLE OF INVENTION: Respiratory Syncytial Virus

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; FILE REFERENCE: 415852000100
; CURRENT APPLICATION NUMBER: US/09/202.035
; CURRENT FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; EARLIER FILING DATE: 1996-06-05
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 49
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-09-202-035-5

Query Match          99.0%; Score 285; DB 16; Length 49;
Best Local Similarity 98.0%; Pred. No. 1.3e-26;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNDFHFEVFNFPVCSICSNPTCWAICKRIPNKKPGKK 49
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 KORQKPPKNPNDFHFEVFNFPVCSICSNPTCWAICKRIPNKKPGKK 49

RESULT 11
US-09-202-035-6
; Sequence 6, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; FILE REFERENCE: 415852000100
; CURRENT APPLICATION NUMBER: US/09/202.035
; CURRENT FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; EARLIER FILING DATE: 1996-06-05
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 49
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-09-202-035-6

Query Match          99.0%; Score 285; DB 16; Length 49;
Best Local Similarity 98.0%; Pred. No. 1.3e-26;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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RESULT 12
US-09-202-035-7
; Sequence 7, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; FILE REFERENCE: 415852000100
; CURRENT APPLICATION NUMBER: US/09/202.035
; CURRENT FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; EARLIER FILING DATE: 1996-06-05
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 49
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-09-202-035-7

Query Match          99.0%; Score 285; DB 16; Length 49;
Best Local Similarity 98.0%; Pred. No. 1.3e-26;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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RESULT 13
US-09-202-035-8
; Sequence 8, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; FILE REFERENCE: 415852000100
; CURRENT APPLICATION NUMBER: US/09/202.035
; CURRENT FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; EARLIER FILING DATE: 1996-06-05
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 49
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-09-202-035-8

Query Match          99.0%; Score 285; DB 16; Length 49;
Best Local Similarity 98.0%; Pred. No. 1.3e-26;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNDFHFEVFNFPVCSICSNPTCWAICKRIPNKKPGKK 49
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RESULT 14
US-08-896-442-4
; Sequence 4, Application US/08896442
; GENERAL INFORMATION:
; APPLICANT: Li, Xiaomao
; APPLICANT: SURIAPRAKESH, Sambhara
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: NUCLEIC ACID VACCINES ENCODING G PROTEIN OF RESPIRATORY
; FILE REFERENCE: 1038-711 MIS
; CURRENT APPLICATION NUMBER: US/08/896,442
; CURRENT FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 232
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-08-896-442-4

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Best Local Similarity 98.0%; Pred. No. 6.4e-26;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 KORONKPPSKFNDFHFEVFNFPVCSICSNNPTCWAICKRIPNKKPGKK 49
Db 83 KORONKPPSKFNDFHFEVFNFPVCSICSNNPTCWAICKRIPNKKPGKK 131

RESULT 15
US-09-272-262-4
; Sequence 4, Application US/09272262
; GENERAL INFORMATION:
; APPLICANT: LI, Xiaomao
; APPLICANT: SURYAPRAKASH, Sambhara
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: NUCLEIC ACID VACCINES ENCODING G PROTEIN OF RESPIRATORY
; TITLE OF INVENTION: SYNCYTIAL VIRUS
; FILE REFERENCE: 1038-923 MIS
; CURRENT APPLICATION NUMBER: US/09/272,262
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 08/896,442
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 232
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-09-272-262-4

Query Match 99.0%; Score 285; DB 16; Length 232;
Best Local Similarity 98.0%; Pred. No. 6.4e-26;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KORONKPPSKFNDFHFEVFNFPVCSICSNNPTCWAICKRIPNKKPGKK 49
Db 83 KORONKPPSKFNDFHFEVFNFPVCSICSNNPTCWAICKRIPNKKPGKK 131

Search completed: May 21, 2001, 14:16:11
Job time: 80 sec

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; OTHER INFORMATION: /product= 011
; OTHER INFORMATION: /note= "sequence 174-187 / name : Gl'A"
US-09-654-289-9

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; OTHER INFORMATION: /product= 011
; OTHER INFORMATION: /note= "sequence 174-187 / name : G1'A"
US-09-654-289-9

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RESULT 5
US-09-654-289-19
; Sequence 19, Application US/09654289
; GENERAL INFORMATION:
; APPLICANT: Binz, Hans
; APPLICANT: N'Guyen, Ngoc Thien
; APPLICANT: Baussant, Thierry
; APPLICANT: Trudel, Michel
; TITLE OF INVENTION: PEPTIDE FRAGMENT OF RESPIRATORY
; TITLE OF INVENTION: SYNCYTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITION CONTAINING IT AND PREPARATION PROCESS
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gordon W. Hueschen
; STREET: 715 The "H" Bldg., 310 East Michigan
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/654,289
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/721,979
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hueschen, Gordon W.
; REGISTRATION NUMBER: 16,157
; REFERENCE/DOCKET NUMBER: PF57PCTUS/dln
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616-382-0030
; TELEFAX: 616-382-2030
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 12
; OTHER INFORMATION: /product= "Orn"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 16
; OTHER INFORMATION: /product= "Orn"
; OTHER INFORMATION: /note= "sequence 171-187 / name : G4'A"
US-09-654-289-19

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Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 23 VPCSISSNNPTCWAICK 39
Db 1 VPDSIDSNPTXWAIX 17

RESULT 6
PCT-US01-04098A-3126
; Sequence 3126, Application PC/TUS0104098A
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
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; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-029
; CURRENT APPLICATION NUMBER: PCT/US01/04098A
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: Not Yet Assigned
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 09/728,422
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 09/693,325
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/663,561
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/654,936
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 09/620,325
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/598,075
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 3960
; SOFTWARE: Custom
; SEQ ID NO 3126
; LENGTH: 1778
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US01-04098A-3126

Query Match 19.3%; Score 55.5; DB 1; Length 1778;
Best Local Similarity 19.1%; Pred. No. 16;
Matches 18; Conservative 12; Mismatches 13; Indels 51; Gaps 4;

Qy 7 PPSKPNDF-----HFEVFN-----FVPCSISS- 29
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Db 1021 PPTQPSQEFVPPATPPARHQWVPDETSICMVCCREHFTMNRHRCRCGLVCCSCT 1080
||:|:|:|

Qy 30 -----NNPT-----CWAICKRIPNKKGKK 49
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Db 1081 KKMVVEGRENPARVCDQCYSYCNKNDVPEPSEK 1114
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RESULT 7
PCT-US01-04098A-1158
; Sequence 1158, Application PC/TUS0104098A
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-029
; CURRENT APPLICATION NUMBER: PCT/US01/04098A
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: Not Yet Assigned
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 09/728,422
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 09/693,325
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/663,561
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/654,936
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 09/620,325
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/598,075
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 3960
; SOFTWARE: Custom
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; OTHER INFORMATION: /product= "Orn"
; OTHER INFORMATION: /note= "sequence 174-187 / name : Gl'AdeltaC"
US-09-654-289-11

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Query Match 18.1%; Score 52; DB 5; Length 39;
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Matches 8; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

RESULT 15
US-09-549-066-57
; Sequence 57, Application US/09549066

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; GENERAL INFORMATION:
; APPLICANT: Yuan, Junying
; APPLICANT: Miura, Masayuki
; TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/549,066
; FILING DATE: 13-APRIL-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/258,287B
; FILING DATE: 10-JUN-1994
; APPLICATION NUMBER: US 08/080,850
; FILING DATE: 24-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugalsky, Lawrence B.
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 0609.3920001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; TELEX: 248636 SSK
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-549-066-57
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Best Local Similarity 32.3%; Pred. No. 32;
Matches 10; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

Qy 2 QRQNKPPSKPNNDHFVFNFPVCSICSNP 32
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Db 260 KHRNKKPDVLHDDTIFKIFNNSNCRSLRNKP 290
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Search completed: May 21, 2001, 14:16:37
Job time: 105 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 21, 2001, 14:17:02 ; Search time 37.42 Seconds

(without alignments)
210.633 Million cell updates/sec

Title: US-09-202-035-1

Perfect score: 49

Sequence: 1 KQKQNKPKSPKPNNDPFEVY.....NPTCWAICKRIPKKGK 49

Scoring table:

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Searched:

1009251 seqs, 160854530 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1009251

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

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245	5	10.2	58	23	US-60-178-308-2049	Sequence 2049, Ap	318	5	10.2	77	23	US-60-194-508-3103	Sequence 3103, Ap
246	5	10.2	58	23	US-60-182-568-610	Sequence 610, App	319	5	10.2	78	16	US-09-270-767-57310	Sequence 57310, A
247	5	10.2	60	16	US-09-252-691-10379	Sequence 10379, A	320	5	10.2	78	23	US-60-182-569-846	Sequence 846, App
248	5	10.2	60	16	US-09-252-691C-10379	Sequence 10379, A	321	5	10.2	79	16	US-09-248-796-24012	Sequence 24012, A
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250	5	10.2	60	23	US-60-182-569-1316	Sequence 1316, Ap	323	5	10.2	79	23	US-60-173-469-1436	Sequence 1436, Ap
251	5	10.2	61	23	US-60-146-055-567	Sequence 567, App	324	5	10.2	79	23	US-60-173-686-1267	Sequence 1267, Ap
252	5	10.2	62	19	US-09-540-236-3169	Sequence 3169, Ap	325	5	10.2	80	1	PCT-US99-22855-1220	Sequence 1220, Ap
253	5	10.2	62	23	US-60-128-476-4267	Sequence 4267, Ap	326	5	10.2	80	16	US-09-248-796-23505	Sequence 23505, A
254	5	10.2	62	23	US-60-147-499-6905	Sequence 6905, Ap	327	5	10.2	80	18	US-09-450-969-5300	Sequence 5300, Ap
255	5	10.2	63	16	US-09-248-796-25607	Sequence 25607, A	328	5	10.2	80	23	US-60-186-656-1338	Sequence 1338, Ap
256	5	10.2	63	23	US-60-170-347-431	Sequence 431, App	329	5	10.2	80	23	US-60-230-445-1474	Sequence 1474, Ap
257	5	10.2	63	23	US-60-188-162-5046	Sequence 5046, Ap	330	5	10.2	81	23	US-60-192-887-1190	Sequence 1190, Ap
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259	5	10.2	64	1	PCT-US99-00108-71	Sequence 71, App	332	5	10.2	82	16	US-09-248-796-22665	Sequence 22665, A
260	5	10.2	64	17	US-09-348-457-71	Sequence 71, App	333	5	10.2	83	16	US-09-417-507-43067	Sequence 43067, A
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262	5	10.2	64	21	US-09-739-907-71	Sequence 71, App	335	5	10.2	84	21	US-09-726-643-66	Sequence 66, App
263	5	10.2	65	1	PCT-US93-04128A-14	Sequence 14, App	336	5	10.2	85	16	US-09-270-767-32622	Sequence 32622, A
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266	5	10.2	65	4	US-08-066-384A-32	Sequence 32, App	339	5	10.2	85	19	US-09-502-698-10	Sequence 10, App
267	5	10.2	65	7	US-08-310-503-14	Sequence 14, App	340	5	10.2	85	23	US-60-198-824-114	Sequence 114, App
268	5	10.2	65	23	US-60-236-359-20604	Sequence 20604, A	341	5	10.2	86	17	US-09-307-890-647	Sequence 647, App
269	5	10.2	66	16	US-09-270-767-61966	Sequence 61966, A	342	5	10.2	86	23	US-60-163-233-3479	Sequence 3479, App
270	5	10.2	66	23	US-60-160-190-1350	Sequence 1350, Ap	343	5	10.2	86	23	US-60-170-430-1870	Sequence 1870, Ap
271	5	10.2	67	1	PCT-US00-00724-635	Sequence 635, App	344	5	10.2	89	23	US-60-138-831-4172	Sequence 4172, App
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274	5	10.2	67	18	US-09-417-507-43356	Sequence 43356, A	347	5	10.2	90	1	PCT-US00-00724-92	Sequence 92, App
275	5	10.2	67	20	US-09-699-146-215	Sequence 215, App	348	5	10.2	90	1	PCT-US99-22855-1219	Sequence 1219, Ap
276	5	10.2	67	23	US-60-160-203-5626	Sequence 5626, Ap	349	5	10.2	90	16	US-09-228-886-92	Sequence 92, App
277	5	10.2	67	23	US-60-160-209-4128	Sequence 4128, Ap	350	5	10.2	92	23	US-60-162-866-92	Sequence 92, App
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281	5	10.2	68	1	PCT-US00-06049-119	Sequence 119, App	354	5	10.2	93	23	US-60-171-881-1638	Sequence 1638, Ap
282	5	10.2	68	1	PCT-US01-01354-18456	Sequence 18456, A	355	5	10.2	94	3	US-07-627-942A-32	Sequence 32, App
283	5	10.2	68	1	PCT-US99-07885-4	Sequence 4, App	356	5	10.2	94	3	US-07-627-942A-106	Sequence 106, App
284	5	10.2	68	16	US-09-288-477-4	Sequence 477, A	357	5	10.2	94	3	US-07-627-942-32	Sequence 32, App
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291	5	10.2	71	20	US-09-611-529-7020	Sequence 7020, Ap	364	5	10.2	96	1	PCT-US94-08207-30	Sequence 30, App
292	5	10.2	72	23	US-60-140-806-846	Sequence 846, App	365	5	10.2	96	1	PCT-US94-08207-30	Sequence 30, App
293	5	10.2	72	23	US-60-142-844-567	Sequence 567, App	366	5	10.2	96	1	PCT-US94-08207-30	Sequence 30, App
294	5	10.2	73	14	US-09-043-861-30	Sequence 30, App	367	5	10.2	96	8	US-08-479-603-24	Sequence 24, App
295	5	10.2	73	15	US-09-120-523-17	Sequence 17, App	368	5	10.2	96	8	US-08-479-603-24	Sequence 24, App
296	5	10.2	73	17	US-09-360-242-17	Sequence 17, App	369	5	10.2	96	9	US-08-558-658-24	Sequence 24, App
297	5	10.2	73	18	US-09-453-851A-17	Sequence 17, App	370	5	10.2	96	10	US-08-622-851A-17	Sequence 17, App
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300	5	10.2	73	23	US-60-177-646-2352	Sequence 2352, Ap	373	5	10.2	96	14	US-09-067-447-24	Sequence 24, App
301	5	10.2	73	23	US-60-187-387-983	Sequence 983, App	374	5	10.2	96	14	US-09-067-447-24	Sequence 24, App
302	5	10.2	74	1	PCT-US01-02723-226	Sequence 226, App	375	5	10.2	96	14	US-09-067-447B-24	Sequence 24, App

376	5	10.2	96	15	US-09-150-813-47	Sequence 47, Appl	449	5	10.2	121	14	US-09-057-963-6	Sequence 6, Appl
377	5	10.2	96	23	US-60-177-646-3965	Sequence 3965, Ap	450	5	10.2	121	14	US-09-057-963A-6	Sequence 6, Appl
378	5	10.2	96	23	US-60-196-174-791	Sequence 791, App	451	5	10.2	121	21	US-09-740-676-7	Sequence 7, Appl
379	5	10.2	97	18	US-09-450-969-5290	Sequence 5290, Ap	452	5	10.2	121	23	US-60-169-867-5209	Sequence 5209, Ap
380	5	10.2	97	23	US-60-196-174-792	Sequence 792, App	453	5	10.2	122	23	US-08-168-091-36	Sequence 36, Appl
381	5	10.2	97	23	US-60-196-718-5229	Sequence 5229, Ap	454	5	10.2	122	8	US-08-483-339-36	Sequence 36, Appl
382	5	10.2	98	23	US-60-171-489-1077	Sequence 1077, Ap	455	5	10.2	122	8	US-08-487-467-36	Sequence 36, Appl
383	5	10.2	98	8	US-08-472-065-188	Sequence 188, App	456	5	10.2	123	19	US-09-583-110-3923	Sequence 3923, Ap
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386	5	10.2	99	23	US-60-163-245-2935	Sequence 2935, Ap	459	5	10.2	126	11	US-08-728-742-10	Sequence 10, Appl
387	5	10.2	99	23	US-60-169-867-6518	Sequence 6518, Ap	460	5	10.2	126	11	US-08-728-742A-10	Sequence 10, Appl
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390	5	10.2	100	8	US-08-472-065B-188	Sequence 188, App	463	5	10.2	127	23	US-60-192-587-940	Sequence 940, App
391	5	10.2	100	23	US-60-140-806-892	Sequence 892, App	464	5	10.2	127	23	US-60-194-091-916	Sequence 916, App
392	5	10.2	100	23	US-60-191-637-29863	Sequence 29863, A	465	5	10.2	128	1	PCT-US00-06823-168	Sequence 168, App
393	5	10.2	101	1	PCT-US00-05883-774	Sequence 774, App	466	5	10.2	128	1	US-60-236-359-15404	Sequence 15404, A
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399	5	10.2	104	13	US-08-993-002A-81178	Sequence 81178, Ap	472	5	10.2	131	1	PCT-US00-05881-444	Sequence 444, App
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401	5	10.2	104	16	US-09-270-767-48394	Sequence 48394, A	474	5	10.2	131	16	US-09-270-767-33643	Sequence 33643, A
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405	5	10.2	105	23	US-60-192-587-939	Sequence 939, App	478	5	10.2	132	16	US-09-228-966-110	Sequence 110, App
406	5	10.2	105	23	US-60-192-587-941	Sequence 941, App	479	5	10.2	132	23	US-60-162-866-110	Sequence 110, App
407	5	10.2	105	23	US-60-194-091-915	Sequence 915, App	480	5	10.2	132	23	US-60-196-710-5877	Sequence 5877, Ap
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411	5	10.2	107	23	US-60-169-868-3825	Sequence 3825, Ap	484	5	10.2	133	8	US-08-461-097-380	Sequence 380, App
412	5	10.2	108	23	US-60-141-856-525	Sequence 525, App	485	5	10.2	133	8	US-08-467-459A-185	Sequence 185, App
413	5	10.2	108	23	US-60-147-499-5726	Sequence 5726, App	486	5	10.2	133	8	US-08-467-459-185	Sequence 185, App
414	5	10.2	108	23	US-60-197-873-19256	Sequence 19256, A	487	5	10.2	133	8	US-08-467-459-639	Sequence 639, App
415	5	10.2	109	1	PCT-US93-09298-35	Sequence 35, Appl	488	5	10.2	133	8	US-08-467-602-380	Sequence 380, App
416	5	10.2	109	23	US-60-140-956-2377	Sequence 2377, Ap	489	5	10.2	133	8	US-08-467-602-380	Sequence 380, App
417	5	10.2	110	14	US-09-085-380A-4	Sequence 4, Appl	490	5	10.2	133	8	US-08-468-731-360	Sequence 360, App
418	5	10.2	110	14	US-09-085-380A-4	Sequence 4, Appl	491	5	10.2	133	13	US-08-993-002A-6361	Sequence 6361, Ap
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421	5	10.2	111	23	US-60-141-863-843	Sequence 843, App	494	5	10.2	133	18	US-09-417-507-37920	Sequence 37920, A
422	5	10.2	112	23	US-60-192-587-942	Sequence 942, App	495	5	10.2	133	23	US-60-168-693-85	Sequence 55, Appl
423	5	10.2	112	23	US-60-194-091-918	Sequence 918, App	496	5	10.2	133	23	US-60-190-065-96	Sequence 96, Appl
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425	5	10.2	115	1	PCT-US97-02318-297	Sequence 297, App	498	5	10.2	134	23	US-60-196-190-910	Sequence 910, App
426	5	10.2	115	13	US-08-903-470-297	Sequence 297, App	499	5	10.2	135	16	US-09-270-767-34805	Sequence 34805, A
427	5	10.2	116	23	US-60-138-830-288	Sequence 288, App	500	5	10.2	135	16	US-09-270-767-50022	Sequence 50022, A
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432	5	10.2	117	23	US-60-142-844-562	Sequence 562, App	505	5	10.2	136	23	US-60-162-247-5067	Sequence 5067, Ap
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434	5	10.2	118	17	US-09-327-750-50	Sequence 50, Appl	507	5	10.2	137	16	US-09-270-767-4806	Sequence 4806, A
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436	5	10.2	118	23	US-60-192-737-696	Sequence 696, App	509	5	10.2	138	16	US-09-252-991A-24037	Sequence 24037, A
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438	5	10.2	120	1	PCT-US00-02237-32	Sequence 32, App	511	5	10.2	138	17	US-09-328-352-8007	Sequence 8007, Ap
439	5	10.2	120	1	PCT-US00-08983-138	Sequence 138, App	512	5	10.2	139	5	US-08-168-091-35	Sequence 35, Appl
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441	5	10.2	120	23	US-60-117-904-6	Sequence 6, Appl	514	5	10.2	139	8	US-08-487-467-35	Sequence 35, Appl
442	5	10.2	121	8	US-08-454-121-7	Sequence 7, Appl	515	5	10.2	140	23	US-60-178-309-997	Sequence 997, App
443	5	10.2	121	8	US-08-482-161-7	Sequence 7, Appl	516	5	10.2	140	23	US-60-194-508-1722	Sequence 1722, Ap
444	5	10.2	121	8	US-08-482-161A-7	Sequence 7, Appl	517	5	10.2	141	23	US-60-196-713-3608	Sequence 3608, Ap
445	5	10.2	121	8	US-08-485-001-7	Sequence 7, Appl	518	5	10.2	141	23	US-60-253-625-2497	Sequence 2497, Ap
446	5	10.2	121	8	US-08-485-001A-7	Sequence 7, Appl	519	5	10.2	141	23	US-60-257-301-3023	Sequence 3023, Ap
447	5	10.2	121	8	US-08-489-666-7	Sequence 7, Appl	520	5	10.2	141	23	US-60-269-308-4045	Sequence 4045, Ap
448	5	10.2	121	8	US-08-489-666A-7	Sequence 7, Appl	521	5	10.2	142	1	PCT-US00-00724-826	Sequence 826, App

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523	5	10.2	142	16	US-09-252-691C-11072	Sequence 11072, A	596	5	10.2	156	8	US-08-467-459A-186	Sequence 186, App
524	5	10.2	142	17	US-09-307-590-444	Sequence 444, App	597	5	10.2	156	8	US-08-467-459-186	Sequence 186, App
525	5	10.2	142	23	US-60-162-866-826	Sequence 826, App	598	5	10.2	156	8	US-08-467-459-357	Sequence 357, App
526	5	10.2	142	23	US-60-173-864-28838	Sequence 28838, A	599	5	10.2	156	8	US-08-467-602-381	Sequence 381, App
527	5	10.2	142	23	US-60-196-713-3606	Sequence 3606, App	600	5	10.2	156	8	US-08-467-602-381	Sequence 381, App
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530	5	10.2	143	21	US-09-733-089-3715	Sequence 3715, App	603	5	10.2	156	19	US-09-583-110-5063	Sequence 5063, App
531	5	10.2	143	21	US-09-733-089-17045	Sequence 17045, A	604	5	10.2	157	13	US-08-993-002A-6363	Sequence 6363, App
532	5	10.2	143	23	US-60-138-831-465	Sequence 465, App	605	5	10.2	157	15	US-09-107-833-3173	Sequence 3173, App
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534	5	10.2	143	23	US-60-191-637-37702	Sequence 37702, A	607	5	10.2	157	16	US-09-248-796-26906	Sequence 26906, A
535	5	10.2	143	23	US-60-191-681-29226	Sequence 29226, A	608	5	10.2	157	16	US-09-270-767-51754	Sequence 51754, A
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555	5	10.2	147	17	US-09-370-838-99	Sequence 99, App	628	5	10.2	159	21	US-09-738-973-98	Sequence 98, App
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570	5	10.2	149	1	PCT-US01-01358-336	Sequence 336, App	643	5	10.2	165	5	US-08-168-091-33	Sequence 33, App
571	5	10.2	149	16	US-09-248-796-17654	Sequence 17654, A	644	5	10.2	165	8	US-08-467-459-427	Sequence 427, App
572	5	10.2	149	16	US-09-270-767-48018	Sequence 48018, A	645	5	10.2	165	8	US-08-467-459-490	Sequence 490, App
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579	5	10.2	151	23	US-60-160-202-4015	Sequence 4015, App	652	5	10.2	166	23	US-60-167-317-11921	Sequence 11921, A
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587	5	10.2	154	8	US-60-173-464-20146	Sequence 20146, A	660	5	10.2	168	8	US-08-467-459-423	Sequence 423, App
588	5	10.2	154	23	US-60-191-637-24560	Sequence 24560, A	661	5	10.2	168	15	US-09-107-532-3745	Sequence 3745, App
589	5	10.2	154	23	US-60-191-681-19337	Sequence 19337, A	662	5	10.2	168	16	US-09-270-767-38425	Sequence 38425, A
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591	5	10.2	155	21	US-09-733-089-14617	Sequence 14617, A	664	5	10.2	168	19	US-09-340-236-2309	Sequence 2309, App
592	5	10.2	155	23	US-60-270-153-175	Sequence 175, App	665	5	10.2	168	23	US-60-128-476-4025	Sequence 4025, App
593	5	10.2	156	8	US-08-411-295F-306	Sequence 306, App	666	5	10.2	169	18	US-09-417-507-44071	Sequence 44071, A
594	5	10.2	156	8	US-08-461-097A-381	Sequence 381, App	667	5	10.2	169	23	US-60-138-684-746	Sequence 746, App

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669	5	10.2	169	23	US-60-177-662-339	Sequence 339, App	742	5	10.2	185	23	US-60-186-661-539	Sequence 539, App
670	5	10.2	170	1	PCT-US98-25247-339	Sequence 339, App	743	5	10.2	185	23	US-60-190-064-109	Sequence 109, App
671	5	10.2	170	1	PCT-US98-25247-339	Sequence 339, App	744	5	10.2	186	9	US-08-561-6722-2	Sequence 2, App11
672	5	10.2	170	15	US-09-107-433-4561	Sequence 4561, Ap	745	5	10.2	187	23	US-60-195-136-1484	Sequence 1484, Ap
673	5	10.2	170	15	US-09-199-637-339	Sequence 339, App	746	5	10.2	188	8	US-08-467-459-431	Sequence 431, App
674	5	10.2	170	15	US-09-199-637A-339	Sequence 339, App	747	5	10.2	188	8	US-08-467-459-494	Sequence 494, App
675	5	10.2	170	19	US-09-517-537-127	Sequence 127, App	748	5	10.2	188	16	US-09-248-796-18779	Sequence 18779, A
676	5	10.2	170	19	US-09-583-110-3193	Sequence 3193, Ap	749	5	10.2	189	16	US-09-270-767-57193	Sequence 57193, A
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679	5	10.2	171	16	US-09-270-767-49380	Sequence 49380, A	752	5	10.2	191	23	US-60-161-933-546	Sequence 546, App
680	5	10.2	171	16	US-09-270-767-54121	Sequence 54121, A	753	5	10.2	191	23	US-60-191-637-36931	Sequence 36931, A
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682	5	10.2	172	19	US-09-583-110-3791	Sequence 3791, Ap	755	5	10.2	193	17	US-09-397-243-4	Sequence 4, App11
683	5	10.2	173	1	PCT-US00-00724-577	Sequence 577, App	756	5	10.2	193	19	US-09-583-110-4576	Sequence 4576, Ap
684	5	10.2	173	6	US-08-209-2048-240	Sequence 240, App	757	5	10.2	194	12	US-08-881-094-17	Sequence 17, App1
685	5	10.2	173	8	US-08-411-295F-166	Sequence 166, App	758	5	10.2	194	23	US-60-186-652-682	Sequence 682, App
686	5	10.2	173	8	US-08-461-097A-240	Sequence 240, App	759	5	10.2	196	6	US-08-209-2048-244	Sequence 244, App
687	5	10.2	173	8	US-08-461-097A-240	Sequence 240, App	760	5	10.2	196	8	US-08-411-295F-170	Sequence 170, App
688	5	10.2	173	8	US-08-467-459-217	Sequence 217, App	761	5	10.2	196	8	US-08-461-097A-244	Sequence 244, App
689	5	10.2	173	8	US-08-467-602-240	Sequence 240, App	762	5	10.2	196	8	US-08-461-097A-244	Sequence 244, App
690	5	10.2	173	8	US-08-467-602-240	Sequence 240, App	763	5	10.2	196	8	US-08-467-459-221	Sequence 221, App
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696	5	10.2	173	23	US-60-194-508-3296	Sequence 3296, Ap	769	5	10.2	196	9	US-08-535-200A-244	Sequence 244, App
697	5	10.2	174	21	US-09-733-089-15197	Sequence 15197, A	770	5	10.2	196	9	US-60-186-652-684	Sequence 684, App
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701	5	10.2	174	23	US-60-186-662-1030	Sequence 1030, Ap	774	5	10.2	197	16	US-09-270-767-52467	Sequence 52467, A
702	5	10.2	174	23	US-60-234-446-1065	Sequence 1065, Ap	775	5	10.2	198	20	US-09-655-758-8	Sequence 2, App11
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704	5	10.2	176	1	PCT-US99-22853B-3622	Sequence 3622, Ap	777	5	10.2	199	8	US-08-467-459-469	Sequence 469, App
705	5	10.2	176	6	US-08-209-2048-236	Sequence 236, App	778	5	10.2	199	18	US-09-417-507-35212	Sequence 35212, A
706	5	10.2	176	8	US-08-411-295F-162	Sequence 162, App	779	5	10.2	200	1	PCT-US00-09465-2	Sequence 2, App11
707	5	10.2	176	8	US-08-461-097A-236	Sequence 236, App	780	5	10.2	200	7	US-08-308-887-1	Sequence 1, App11
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719	5	10.2	176	23	US-60-196-710-5195	Sequence 5195, Ap	792	5	10.2	205	1	PCT-US98-14371-4	Sequence 4, App11
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725	5	10.2	180	16	US-09-252-691-6456	Sequence 6456, Ap	798	5	10.2	207	8	US-08-411-295F-208	Sequence 208, App
726	5	10.2	180	16	US-09-252-691C-6456	Sequence 6456, Ap	799	5	10.2	207	8	US-08-467-459-259	Sequence 259, App
727	5	10.2	181	16	US-09-252-991A-25104	Sequence 25104, A	800	5	10.2	207	8	US-08-461-097A-219	Sequence 219, App
728	5	10.2	181	18	US-09-417-507-27249	Sequence 27249, A	801	5	10.2	207	8	US-08-461-097A-282	Sequence 282, App
729	5	10.2	181	21	US-09-791-279-203	Sequence 203, App	802	5	10.2	207	8	US-08-461-097-219	Sequence 219, App
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737	5	10.2	184	16	US-09-417-507-29946	Sequence 29946, A	810	5	10.2	207	8	US-08-468-731A-282	Sequence 282, App
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814	5	10.2	207	8	US-08-469-549-392	Sequence 292, App
815	5	10.2	207	9	US-08-535-200A-219	Sequence 219, App
816	5	10.2	207	9	US-08-535-200A-282	Sequence 282, App
817	5	10.2	207	18	US-09-417-507-35610	Sequence 35610, A
818	5	10.2	208	16	US-09-270-767-3250	Sequence 3250, A
819	5	10.2	208	16	US-09-270-767-47757	Sequence 47757, A
820	5	10.2	208	23	US-60-191-637-21173	Sequence 21173, A
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822	5	10.2	209	16	US-09-270-767-57900	Sequence 57900, A
823	5	10.2	210	6	US-08-209-204B-215	Sequence 215, App
824	5	10.2	210	6	US-08-209-204B-278	Sequence 278, App
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826	5	10.2	210	8	US-08-411-295F-204	Sequence 204, App
827	5	10.2	210	8	US-08-461-097A-215	Sequence 215, App
828	5	10.2	210	8	US-08-461-097A-278	Sequence 278, App
829	5	10.2	210	8	US-08-461-097-215	Sequence 215, App
830	5	10.2	210	8	US-08-461-097-278	Sequence 278, App
831	5	10.2	210	8	US-08-467-459-192	Sequence 192, App
832	5	10.2	210	8	US-08-467-459-255	Sequence 255, App
833	5	10.2	210	8	US-08-467-602-215	Sequence 215, App
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836	5	10.2	210	8	US-08-467-602-278	Sequence 278, App
837	5	10.2	210	8	US-08-468-731A-215	Sequence 215, App
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866	5	10.2	217	16	US-09-215-887-3	Sequence 3, App1
867	5	10.2	218	19	US-09-595-329A-348	Sequence 348, App1
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869	5	10.2	218	23	US-60-194-508-1942	Sequence 1942, App
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874	5	10.2	220	1	PCT-US99-22853B-1323	Sequence 1323, App
875	5	10.2	220	7	US-08-375-992A-4	Sequence 4, App1
876	5	10.2	220	8	US-08-472-679B-4	Sequence 4, App1
877	5	10.2	220	8	US-08-472-679D-4	Sequence 4, App1
878	5	10.2	220	8	US-08-486-237A-4	Sequence 4, App1
879	5	10.2	220	11	US-08-759-625-93	Sequence 93, App1
880	5	10.2	220	12	US-08-823-745-93	Sequence 93, App1
881	5	10.2	220	13	US-08-993-001-95	Sequence 95, App1
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883	5	10.2	220	21	US-09-773-370-58	Sequence 58, App1
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886	5	10.2	222	8	US-08-467-459-473	Sequence 473, App
887	5	10.2	222	16	US-09-252-991A-21848	Sequence 21848, A
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893	5	10.2	225	16	US-09-252-691C-30156	Sequence 30156, A
894	5	10.2	225	21	US-09-709-947-5	Sequence 5, App1
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896	5	10.2	226	3	PCT-US97-14436-509	Sequence 509, App
897	5	10.2	226	3	US-07-751-896-14	Sequence 14, App1
898	5	10.2	226	3	US-07-837-773-26	Sequence 26, App1
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901	5	10.2	226	13	US-08-911-503A-509	Sequence 509, App
902	5	10.2	226	13	US-08-942-888-41	Sequence 41, App1
903	5	10.2	226	13	US-08-943-570-41	Sequence 41, App1
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905	5	10.2	226	13	US-08-968-838A-35	Sequence 35, App1
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910	5	10.2	228	16	US-09-252-691C-10174	Sequence 10174, A
911	5	10.2	229	12	US-08-836-687-31	Sequence 31, App1
912	5	10.2	229	18	US-09-417-507-43529	Sequence 43529, A
913	5	10.2	230	6	US-08-209-204B-223	Sequence 223, App
914	5	10.2	230	6	US-08-209-204B-286	Sequence 286, App
915	5	10.2	230	8	US-08-411-295F-119	Sequence 119, App
916	5	10.2	230	8	US-08-411-295F-212	Sequence 212, App
917	5	10.2	230	8	US-08-461-097A-223	Sequence 223, App
918	5	10.2	230	8	US-08-461-097A-286	Sequence 286, App
919	5	10.2	230	8	US-08-461-097-223	Sequence 223, App
920	5	10.2	230	8	US-08-461-097-286	Sequence 286, App
921	5	10.2	230	8	US-08-467-459-200	Sequence 200, App
922	5	10.2	230	8	US-08-467-459-263	Sequence 263, App
923	5	10.2	230	8	US-08-467-602-223	Sequence 223, App
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932	5	10.2	230	8	US-08-468-731-286	Sequence 286, App
933	5	10.2	230	9	US-08-535-200A-223	Sequence 223, App
934	5	10.2	230	9	US-08-535-200A-286	Sequence 286, App
935	5	10.2	230	18	US-09-417-507-27656	Sequence 27656, A
936	5	10.2	231	1	PCT-US94-05670-35	Sequence 35, App1
937	5	10.2	231	1	PCT-US94-05670-35	Sequence 35, App1
938	5	10.2	231	4	US-08-066-364A-35	Sequence 35, App1
939	5	10.2	231	4	US-08-085-126-162	Sequence 162, App
940	5	10.2	231	4	US-08-438-114-162	Sequence 162, App
941	5	10.2	231	17	US-09-311-940-6	Sequence 6, App1
942	5	10.2	231	18	US-09-488-725A-2651	Sequence 2651, App
943	5	10.2	232	18	US-09-417-507-37282	Sequence 37282, App
944	5	10.2	232	18	US-09-489-039A-11927	Sequence 11927, A
945	5	10.2	233	11	US-08-761-066-442	Sequence 442, App
946	5	10.2	233	13	US-08-993-002A-8217	Sequence 8217, App
947	5	10.2	234	18	US-09-488-725A-6497	Sequence 6497, App
948	5	10.2	235	18	US-09-417-507-33237	Sequence 33237, A
949	5	10.2	235	19	US-09-509-612-16	Sequence 16, App1
950	5	10.2	236	19	US-09-509-612-17	Sequence 17, App1
951	5	10.2	236	19	US-09-509-612-18	Sequence 18, App1
952	5	10.2	236	19	US-09-509-612-19	Sequence 19, App1
953	5	10.2	236	19	US-09-509-612-20	Sequence 20, App1
954	5	10.2	237	16	US-09-270-767-53388	Sequence 53388, A
955	5	10.2	237	16	US-09-270-767-53388	Sequence 53388, A
956	5	10.2	237	18	US-09-468-725A-6223	Sequence 6223, App
957	5	10.2	237	23	US-60-177-646-2740	Sequence 2740, App
958	5	10.2	238	3	US-07-598-877-6	Sequence 6, App1
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RESULT      2
US-09-202-035-32
; Sequence 32, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; TITLE OF INVENTION: Respiratory Syncytial Virus
; FILE REFERENCE: 415852000100
; CURRENT APPLICATION NUMBER: US/09/202,035
; EARLIER FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 49
; TYPE: PRF
; ORGANISM: respiratory syncytial virus
US-09-202-035-32

Query Match /           100.0%; Score 49; DB 16; Length 49;
Best Local Similarity 100.0%; Pred. No. 1,Se-45;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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RESULT      3
US-09-202-035-36
; Sequence 36, Application US/09202035
; GENERAL INFORMATION:
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? TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
? TITLE OF INVENTION: Respiratory Syncytial Virus
? FILE REFERENCE: 415852000100
? CURRENT APPLICATION NUMBER: US/09/202_035
? CURRENT FILING DATE: 1998-12-17
? EARLIER APPLICATION NUMBER: PCT/AU97/00351
? EARLIER FILING DATE: 1997-06-04
? EARLIER APPLICATION NUMBER: AU PO 0265
? EARLIER FILING DATE: 1996-06-05
? NUMBER OF SEQ ID NOS: 44
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 36
? LENGTH: 49
? TYPE: PRT
? ORGANISM: respiratory syncytial virus
? FEATURE:
? NAME/KEY: SITE
? LOCATION: (1)
? OTHER INFORMATION: acetylation
? FEATURE:
? NAME/KEY: SITE
? LOCATION: (49)
? OTHER INFORMATION: amidation
? US-09-202-035-36

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Query Match	100.0%;	Score 49;	DB 16;	Length 49;
Best Local Similarity	100.0%;	Pred. No. 1,5e-45;		
Matches 49;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
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Db 1 KOROKPPSKPNNDFHFVFNFPSCISNNPTCWAICKRIPNKKPGKK 49

RESULT 4
US-09-202-035-40

Sequence 40, Application US/09202035
GENERAL INFORMATION:
APPLICANT: Jeffrey John Gorman
TITLE OF INVENTION: Viral peptides with Structural Homology to Protein G of
FILE REFERENCE: 41585200100
CURRENT FILING DATE: 1998-12-17
EARLIER FILING DATE: 1997-06-04
EARLIER APPLICATION NUMBER: PCT/AU97/00351
EARLIER FILING DATE: 1997-06-04
EARLIER APPLICATION NUMBER: AU PO 0265
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 40
LENGTH: 49
TYPE: PRT
ORGANISM: respiratory syncytial virus
FEATURE:
NAME/KEY: SITE
LOCATION: (1)
OTHER INFORMATION: fluorescein isothiocarbanyl beta-alanine
FEATURE:
OTHER INFORMATION: derivatisation
NAME/KEY: SITE
LOCATION: (49)
OTHER INFORMATION: amidation
US-09-202-035-40

Query Match 100.0%; Score 49; DB 16; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.5e-45;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KOROKPPSKPNNDFHFVFNFPSCISNNPTCWAICKRIPNKKPGKK 49
Db 1 KOROKPPSKPNNDFHFVFNFPSCISNNPTCWAICKRIPNKKPGKK 49

RESULT 5
US-09-202-035-42

Sequence 42, Application US/09202035
GENERAL INFORMATION:
APPLICANT: Jeffrey John Gorman
TITLE OF INVENTION: Viral peptides with Structural Homology to Protein G of
FILE REFERENCE: 41585200100
CURRENT FILING DATE: US/09/202, 035
CURRENT FILING DATE: 1998-12-17
EARLIER FILING DATE: PCT/AU97/00351
EARLIER FILING DATE: 1997-06-04
EARLIER APPLICATION NUMBER: AU PO 0265
EARLIER FILING DATE: 1996-06-05
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 42
LENGTH: 49
TYPE: PRT
ORGANISM: respiratory syncytial virus
FEATURE:
NAME/KEY: SITE
LOCATION: (1)
OTHER INFORMATION: benzoyl benzylamide derivatisation
FEATURE:
NAME/KEY: SITE
LOCATION: (49)
OTHER INFORMATION: amidation

US-09-202-035-42

Query Match 100.0%; Score 49; DB 16; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.5e-45;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KOROKPPSKPNNDFHFVFNFPSCISNNPTCWAICKRIPNKKPGKK 49
Db 1 KOROKPPSKPNNDFHFVFNFPSCISNNPTCWAICKRIPNKKPGKK 49

RESULT 6
US-09-202-035-43

Sequence 43, Application US/09202035
GENERAL INFORMATION:
APPLICANT: Jeffrey John Gorman
TITLE OF INVENTION: Viral peptides with Structural Homology to Protein G of
FILE REFERENCE: 41585200100
CURRENT FILING DATE: US/09/202, 035
EARLIER FILING DATE: PCT/AU97/00351
EARLIER FILING DATE: 1997-06-04
EARLIER APPLICATION NUMBER: AU PO 0265
EARLIER FILING DATE: 1996-06-05
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 43
LENGTH: 49
TYPE: PRT
ORGANISM: respiratory syncytial virus
FEATURE:
NAME/KEY: SITE
LOCATION: (1)
OTHER INFORMATION: biotinyl amide derivatisation
FEATURE:
NAME/KEY: SITE
LOCATION: (49)
OTHER INFORMATION: amidation
US-09-202-035-43

Query Match 100.0%; Score 49; DB 16; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.5e-45;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KOROKPPSKPNNDFHFVFNFPSCISNNPTCWAICKRIPNKKPGKK 49
Db 1 KOROKPPSKPNNDFHFVFNFPSCISNNPTCWAICKRIPNKKPGKK 49

RESULT 7
US-60-208-701-2

Sequence 2, Application US/60208701
GENERAL INFORMATION:
APPLICANT: Portner, Allen
TITLE OF INVENTION: VACCINE AND GENE THERAPY VECTOR AND METHODS OF USE
FILE REFERENCE: 1340-1-030P
CURRENT FILING DATE: US/60/208, 701
CURRENT FILING DATE: 2000-06-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 298
TYPE: PRT
ORGANISM: Paramyxoviridae pneumovirinae pneumovirus respiratory syncytial virus
US-60-208-701-2

Query Match 100.0%; Score 49; DB 23; Length 298;

Best Local Similarity 100.0%; Pred. No. 7.5e-45;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 149 KORONKPPSKPNDHFHEVNFVPCISCSNNPTCMAICKRIPKPKGK 197

RESULT 8

US-09-202-035-3
; Sequence 3: Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; FILE REFERENCE: 415852000100
; CURRENT APPLICATION NUMBER: US/09/202,035
; EARLIER FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; EARLIER FILING DATE: 1996-06-05
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 3
; LENGTH: 49
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-09-202-035-3

Query Match 98.0%; Score 48; DB 16; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.8e-44;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 KORONKPPSKPNDHFHEVNFVPCISCSNNPTCMAICKRIPKPKGK 48

RESULT 9

US-09-202-035-8
; Sequence 8: Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; FILE REFERENCE: 415852000100
; CURRENT APPLICATION NUMBER: US/09/202,035
; EARLIER FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; EARLIER FILING DATE: 1996-06-05
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 8
; LENGTH: 49
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-09-202-035-8

Query Match 98.0%; Score 48; DB 16; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.8e-44;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 10

US-09-202-035-4
; Sequence 4: Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; FILE REFERENCE: 415852000100
; CURRENT APPLICATION NUMBER: US/09/202,035
; EARLIER FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 4
; LENGTH: 49
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-09-202-035-4

Query Match 93.9%; Score 46; DB 16; Length 49;
Best Local Similarity 100.0%; Pred. No. 2.6e-42;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 4 QNKPPSKPNDHFHEVNFVPCISCSNNPTCMAICKRIPKPKGK 49

RESULT 11

US-09-202-035-37
; Sequence 37: Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; FILE REFERENCE: 415852000100
; CURRENT APPLICATION NUMBER: US/09/202,035
; EARLIER FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; EARLIER FILING DATE: 1996-06-05
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 37
; LENGTH: 42
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: acetylation
; NAME/KEY: SITE
; LOCATION: (42)
; OTHER INFORMATION: amidation
US-09-202-035-37

Query Match 85.7%; Score 42; DB 16; Length 42;
Best Local Similarity 100.0%; Pred. No. 4.7e-38;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 KORONKPPSKPNDHFHEVNFVPCISCSNNPTCMAICKRIP 42

RESULT 12

US-09/462

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; Sequence 9, Application US/09462918
; GENERAL INFORMATION:
; APPLICANT: PIERRE FABRE MEDICAMENT
; TITLE OF INVENTION: RSV EPITOPES AND ANTIBODIES COMPRISING THEM, USEFUL IN DIAGNOSIS
; FILE REFERENCE: 339188/D17017
; CURRENT APPLICATION NUMBER: US/09/462,918
; CURRENT FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: FR 97 09079
; PRIOR FILING DATE: 1997-07-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentln Vers. 2.0
; SEQ ID NO 9
; LENGTH: 43
; TYPE: PRT
; ORGANISM: DERIVATED FROM G PROTEIN OF RSV (RESPIRATORY SYNCYTIAL VIRUS).
; FEATURE:
; OTHER INFORMATION: G8a. The first amino acid residue corresponds to the position aa
US/09/462,918-9
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Query Match          81.6%; Score 40; DB 18; Length 43;
Best Local Similarity 100.0%; Pred. No. 6.9e-36;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 KPNDHFEEVFNFPVPCSSNNPTCWAICRIPNKKPGKK 40
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US-09-202-035-2
; Sequence 2, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; FILE REFERENCE: 415852000100
; CURRENT APPLICATION NUMBER: US/09/202,035
; CURRENT FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; EARLIER FILING DATE: 1996-06-05
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 2
; LENGTH: 49
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-09-202-035-2
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Query Match          81.6%; Score 40; DB 16; Length 49;
Best Local Similarity 100.0%; Pred. No. 7.8e-36;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 10 KPNDHFEEVFNFPVPCSSNNPTCWAICRIPNKKPGKK 49
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US-09-202-035-5
; Sequence 5, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; FILE REFERENCE: 415852000100
; CURRENT APPLICATION NUMBER: US/09/202,035
; CURRENT FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
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; EARLIER APPLICATION NUMBER: AU PO 0265
; EARLIER FILING DATE: 1996-06-05
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 5
; LENGTH: 49
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-09-202-035-5
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Best Local Similarity 100.0%; Pred. No. 7.8e-36;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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US-09-202-035-6
; Sequence 6, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; FILE REFERENCE: 415852000100
; CURRENT APPLICATION NUMBER: US/09/202,035
; CURRENT FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; EARLIER FILING DATE: 1996-06-05
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 6
; LENGTH: 49
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-09-202-035-6
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Query Match          81.6%; Score 40; DB 16; Length 49;
Best Local Similarity 100.0%; Pred. No. 7.8e-36;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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GenCore version 4.5
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OM protein - protein search, using sw model

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Title: US-09-202-035-1

Perfect score: 49
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Gapop 60.0 , Gapext 60.0

Searched: 41203 seqs, 7056526 residues

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Minimum DB seq length: 0

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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	5	10.2	14	US-09-654-289-11	Sequence 11, Appl1
7	5	10.2	17	US-09-654-289-19	Sequence 19, Appl1
8	5	10.2	17	US-09-654-289-20	Sequence 20, Appl1
9	5	10.2	26	US-09-722-329-107	Sequence 107, App
10	5	10.2	36	PCT-US00-01979A-264	Sequence 264, App
11	5	10.2	36	US-09-493-795A-264	Sequence 264, App
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15	5	10.2	75	PCT-US01-01339-3043	Sequence 3043, Ap
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17	5	10.2	89	PCT-US01-01329-1393	Sequence 1393, Ap
18	5	10.2	96	PCT-US01-12305-3	Sequence 3, Appl1
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106	4	8.2	37	5	US-09-813-345-7	Sequence 7, App11	179	4	8.2	73	1	PCT-US01-11988-2161	Sequence 2161, Ap
107	4	8.2	37	5	US-09-813-345-8	Sequence 8, App11	180	4	8.2	73	5	US-09-739-449-9323	Sequence 9323, Ap
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115	4	8.2	40	5	US-09-801-436-300	Sequence 300, App1	188	4	8.2	76	5	US-09-187-693-37	Sequence 36, App1
116	4	8.2	40	5	US-09-308-823A-59	Sequence 59, App1	189	4	8.2	76	5	US-09-60-248-505-1315	Sequence 37, App1
117	4	8.2	42	1	PCT-US01-11988-633	Sequence 633, App	190	4	8.2	77	6	US-09-833-245-943	Sequence 943, App
118	4	8.2	42	1	PCT-US01-11988-635	Sequence 635, App	191	4	8.2	78	1	PCT-US01-01339-4526	Sequence 4526, Ap
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120	4	8.2	42	5	US-09-833-245-635	Sequence 635, App	193	4	8.2	81	1	PCT-US01-01339-5105	Sequence 5105, Ap
121	4	8.2	43	5	US-09-601-600-256	Sequence 256, App	194	4	8.2	81	5	US-09-640-211A-831	Sequence 831, App
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124	4	8.2	44	1	PCT-US01-01321-1429	Sequence 1419, Ap	197	4	8.2	82	1	PCT-US01-11988-339	Sequence 339, App
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139	4	8.2	54	1	PCT-US01-01329-1941	Sequence 1941, Ap	212	4	8.2	87	1	PCT-US01-01339-1722	Sequence 1722, Ap
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141	4	8.2	55	1	PCT-US01-11988-882	Sequence 882, App	214	4	8.2	88	5	US-09-739-449-12531	Sequence 12531, A
142	4	8.2	55	1	PCT-US01-01321-1542	Sequence 1542, Ap	215	4	8.2	88	5	US-09-817-427-367	Sequence 367, App
143	4	8.2	55	5	US-09-817-427-323	Sequence 323, App	216	4	8.2	88	5	US-09-833-343-215	Sequence 215, App
144	4	8.2	55	5	US-09-833-245-882	Sequence 882, App	217	4	8.2	89	1	PCT-US01-01350-59	Sequence 59, App1
145	4	8.2	55	6	US-60-248-505-910	Sequence 910, App	218	4	8.2	89	1	PCT-US01-01339-2989	Sequence 2989, Ap
146	4	8.2	56	1	PCT-US01-01339-3442	Sequence 3442, Ap	219	4	8.2	89	1	PCT-US01-01339-4550	Sequence 4550, Ap
147	4	8.2	56	1	PCT-US01-01339-5018	Sequence 5018, Ap	220	4	8.2	89	1	PCT-US01-11988-1838	Sequence 1838, Ap
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151	4	8.2	58	1	PCT-US01-01339-3679	Sequence 3679, Ap	224	4	8.2	90	5	US-09-640-211A-1008	Sequence 1008, Ap
152	4	8.2	58	1	PCT-US01-01329-1113	Sequence 1113, Ap	225	4	8.2	90	5	PCT-US01-01339-5013	Sequence 5013, Ap
153	4	8.2	61	5	US-09-640-211A-2340	Sequence 2340, Ap	226	4	8.2	91	1	PCT-US01-01339-5352	Sequence 5352, Ap
154	4	8.2	62	1	PCT-US01-11988-139	Sequence 139, App	227	4	8.2	93	1	PCT-US01-01339-1977	Sequence 1977, Ap
155	4	8.2	62	1	PCT-US01-11988-140	Sequence 140, App	228	4	8.2	93	5	US-09-640-211A-751	Sequence 751, App
156	4	8.2	62	5	US-09-739-449-12601	Sequence 12601, A	229	4	8.2	94	5	US-09-308-828A-449	Sequence 449, App
157	4	8.2	62	5	US-09-833-245-139	Sequence 139, App	230	4	8.2	95	1	PCT-US01-01339-3472	Sequence 3472, Ap
158	4	8.2	62	5	US-09-833-245-140	Sequence 140, App	231	4	8.2	95	1	PCT-US01-01339-5175	Sequence 5175, Ap
159	4	8.2	63	1	PCT-US01-01339-4529	Sequence 4529, Ap	232	4	8.2	95	1	PCT-US01-01321-1058	Sequence 1058, Ap
160	4	8.2	63	1	PCT-US01-04098A-3268	Sequence 3268, Ap	233	4	8.2	96	6	US-60-248-505-1141	Sequence 1141, Ap
161	4	8.2	63	1	PCT-US01-01329-1786	Sequence 1786, Ap	234	4	8.2	96	1	PCT-US01-11988-943	Sequence 943, App
162	4	8.2	63	5	US-09-739-449-12863	Sequence 12863, A	235	4	8.2	96	1	PCT-US01-11988-944	Sequence 944, App
163	4	8.2	65	1	PCT-US00-35017A-989	Sequence 989, App	236	4	8.2	96	1	PCT-US01-01335-281	Sequence 281, App
164	4	8.2	65	5	US-09-739-449-12478	Sequence 12478, A	237	4	8.2	96	5	US-09-308-828A-376	Sequence 376, App
165	4	8.2	66	1	PCT-US01-01350-96	Sequence 96, App1	238	4	8.2	96	5	US-09-833-245-943	Sequence 943, App
166	4	8.2	67	5	US-09-243-675-10	Sequence 10, App1	239	4	8.2	96	5	US-09-833-245-944	Sequence 944, App
167	4	8.2	67	5	US-09-243-675-11	Sequence 11, App1	240	4	8.2	97	1	PCT-US01-01339-3940	Sequence 3940, Ap
168	4	8.2	67	5	US-09-345-236B-47	Sequence 47, App1	241	4	8.2	97	1	PCT-US01-01339-1363	Sequence 1363, Ap
169	4	8.2	68	1	PCT-US01-01350-118	Sequence 118, App1	242	4	8.2	97	1	PCT-US01-01312-901	Sequence 901, App
170	4	8.2	68	1	PCT-US01-11988-175	Sequence 175, App	243	4	8.2	97	5	US-09-310-707A-16	Sequence 16, App1
171	4	8.2	68	1	PCT-US01-01312-885	Sequence 885, App	244	4	8.2	99	1	PCT-US01-01350-109	Sequence 109, App
172	4	8.2	68	1	PCT-US01-01312-1194	Sequence 1194, Ap	245	4	8.2	99	1	PCT-US00-30036A-133	Sequence 133, App
173	4	8.2	68	5	US-09-833-245-175	Sequence 175, App	246	4	8.2	99	1	PCT-US01-11988-720	Sequence 720, App

247	4	8.2	99	1	PCT-US01-04098A-3896	Sequence 3896, Ap	320	4	8.2	119	5	US-09-155-739-12	Sequence 12, Appl
248	4	8.2	99	5	US-09-833-245-720	Sequence 720, Ap	321	4	8.2	119	5	US-09-155-739-13	Sequence 13, Appl
249	4	8.2	100	1	PCT-US01-04098A-3591	Sequence 3591, Ap	322	4	8.2	120	1	PCT-US01-04098A-1121	Sequence 1121, Ap
250	4	8.2	101	1	PCT-US01-01321-1159	Sequence 1159, Ap	323	4	8.2	120	1	PCT-US01-04098A-3089	Sequence 3089, Ap
251	4	8.2	101	5	US-09-469-200-10	Sequence 10, Appl	324	4	8.2	120	5	US-09-739-449-10718	Sequence 10718, A
252	4	8.2	103	5	US-09-739-449-10710	Sequence 10710, A	325	4	8.2	120	5	US-09-640-211A-2171	Sequence 2171, Ap
253	4	8.2	104	1	PCT-US01-01339-5171	Sequence 5171, Ap	326	4	8.2	121	1	PCT-US01-01339-4538	Sequence 4538, Ap
254	4	8.2	104	5	US-09-147-443D-28	Sequence 28, Appl	327	4	8.2	121	1	PCT-US01-01329-1795	Sequence 1795, Ap
255	4	8.2	105	1	PCT-US01-01310-91	Sequence 91, Appl	328	4	8.2	121	5	US-09-836-377-208	Sequence 208, Ap
256	4	8.2	105	5	US-09-187-693-40	Sequence 40, Appl	329	4	8.2	122	1	PCT-US00-35017A-1039	Sequence 1039, Ap
257	4	8.2	105	5	US-09-187-693-42	Sequence 42, Appl	330	4	8.2	122	5	US-09-739-449-1725	Sequence 12725, A
258	4	8.2	105	5	US-09-187-693-44	Sequence 44, Appl	331	4	8.2	123	1	PCT-US01-01339-2944	Sequence 2944, Ap
259	4	8.2	105	5	US-09-187-693-50	Sequence 50, Appl	332	4	8.2	123	1	PCT-US01-01339-3559	Sequence 3559, Ap
260	4	8.2	105	5	US-09-187-693-52	Sequence 52, Appl	333	4	8.2	123	5	US-09-640-211A-934	Sequence 934, Ap
261	4	8.2	105	5	US-09-187-693-54	Sequence 54, Appl	334	4	8.2	123	5	US-09-155-739-11	Sequence 11, Appl
262	4	8.2	105	5	US-09-147-443D-12	Sequence 12, Appl	335	4	8.2	124	5	US-09-640-679-20	Sequence 20, Appl
263	4	8.2	105	5	US-09-147-443D-16	Sequence 16, Appl	336	4	8.2	125	1	PCT-US01-01339-4975	Sequence 4975, Ap
264	4	8.2	105	5	US-09-147-443D-24	Sequence 24, Appl	337	4	8.2	125	1	PCT-US01-01339-2256	Sequence 2256, Ap
265	4	8.2	105	5	US-09-147-443D-52	Sequence 52, Appl	338	4	8.2	125	5	US-09-647-468-159	Sequence 159, Ap
266	4	8.2	105	5	US-09-147-443D-56	Sequence 56, Appl	339	4	8.2	125	5	US-09-647-468-160	Sequence 160, Ap
267	4	8.2	105	5	US-09-147-443D-60	Sequence 60, Appl	340	4	8.2	125	5	US-09-833-245-2256	Sequence 2256, Ap
268	4	8.2	105	5	US-09-147-443D-64	Sequence 64, Appl	341	4	8.2	126	1	PCT-US01-01339-4786	Sequence 4786, Ap
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271	4	8.2	106	1	PCT-US01-01339-4515	Sequence 4515, Ap	344	4	8.2	126	5	US-09-155-739-15	Sequence 15, Appl
272	4	8.2	106	1	PCT-US01-01329-1772	Sequence 1772, Ap	345	4	8.2	126	5	US-09-155-739-15	Sequence 2, Appl
273	4	8.2	106	5	US-09-817-427-573	Sequence 573, Ap	346	4	8.2	127	1	PCT-US01-08117-83	Sequence 83, Appl
274	4	8.2	106	5	US-09-147-443D-4	Sequence 4, Appl	347	4	8.2	127	5	US-09-647-468-179	Sequence 179, Ap
275	4	8.2	106	5	US-09-147-443D-8	Sequence 8, Appl	348	4	8.2	127	5	US-09-647-468-180	Sequence 180, Ap
276	4	8.2	106	5	US-09-147-443D-20	Sequence 20, Appl	349	4	8.2	127	5	US-09-647-468-181	Sequence 181, Ap
277	4	8.2	106	5	US-09-147-443D-32	Sequence 32, Appl	350	4	8.2	127	5	US-09-647-468-182	Sequence 182, Ap
278	4	8.2	106	5	US-09-155-739-5	Sequence 5, Appl	351	4	8.2	127	5	US-09-640-211A-1151	Sequence 1151, Ap
279	4	8.2	107	1	PCT-US01-01339-5132	Sequence 5132, Ap	352	4	8.2	129	5	US-09-739-449-10612	Sequence 10612, A
280	4	8.2	107	5	US-09-187-693-48	Sequence 48, Appl	353	4	8.2	129	5	US-09-640-211A-772	Sequence 772, Ap
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282	4	8.2	107	5	US-09-647-468-93	Sequence 93, Appl	355	4	8.2	130	5	US-09-155-739-45	Sequence 45, Appl
283	4	8.2	107	5	US-09-647-468-99	Sequence 99, Appl	356	4	8.2	130	1	PCT-US01-01339-4534	Sequence 4534, Ap
284	4	8.2	107	5	US-09-647-468-101	Sequence 101, Ap	357	4	8.2	130	1	PCT-US01-01329-1791	Sequence 1791, Ap
285	4	8.2	107	5	US-09-647-468-107	Sequence 107, Ap	358	4	8.2	130	1	PCT-US01-01332-803	Sequence 803, Ap
286	4	8.2	107	5	US-09-647-468-145	Sequence 145, Ap	359	4	8.2	130	1	PCT-US01-01332-1151	Sequence 1151, Ap
287	4	8.2	107	5	US-09-647-468-146	Sequence 146, Ap	360	4	8.2	131	5	US-09-825-414-58	Sequence 58, Appl
288	4	8.2	107	5	US-09-473-018-1	Sequence 1, Appl	361	4	8.2	132	5	PCT-US01-04098A-1033	Sequence 1033, Ap
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290	4	8.2	108	6	US-60-248-505-1292	Sequence 1292, Ap	363	4	8.2	132	6	US-60-248-505-997	Sequence 997, Ap
291	4	8.2	110	1	PCT-US01-01339-4630	Sequence 4630, Ap	364	4	8.2	132	6	PCT-US01-11663-412	Sequence 412, Ap
292	4	8.2	110	1	PCT-US01-01329-1887	Sequence 1887, Ap	365	4	8.2	133	1	PCT-US01-01312-724	Sequence 724, Ap
293	4	8.2	110	1	PCT-US01-01329-1887	Sequence 1887, Ap	366	4	8.2	134	1	PCT-US01-01312-1128	Sequence 1128, Ap
294	4	8.2	110	5	US-09-815-229-3	Sequence 23, Appl	367	4	8.2	134	1	PCT-US01-01332-926	Sequence 926, Ap
295	4	8.2	110	5	US-09-602-709-23	Sequence 23, Appl	368	4	8.2	134	1	PCT-US01-01332-1201	Sequence 1201, Ap
296	4	8.2	110	5	US-09-602-709-24	Sequence 24, Appl	369	4	8.2	134	1	PCT-US01-01332-1201	Sequence 1201, Ap
297	4	8.2	110	5	US-09-602-709-25	Sequence 25, Appl	370	4	8.2	135	1	PCT-US01-01339-4759	Sequence 4759, Ap
298	4	8.2	110	5	US-09-380-910-12	Sequence 12, Appl	371	4	8.2	135	1	PCT-US01-01312-645	Sequence 645, Ap
299	4	8.2	111	1	PCT-US01-01339-5127	Sequence 5127, Ap	372	4	8.2	135	5	US-09-640-211A-665	Sequence 665, Ap
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301	4	8.2	113	1	PCT-US01-11988-1902	Sequence 1902, Ap	374	4	8.2	136	5	US-09-809-391-385	Sequence 385, Ap
302	4	8.2	113	5	US-09-833-245-1902	Sequence 1902, Ap	375	4	8.2	136	5	US-09-640-211A-189	Sequence 189, Ap
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304	4	8.2	115	1	PCT-US01-04098A-1810	Sequence 1810, Ap	377	4	8.2	138	4	US-08-934-000-11	Sequence 11, Appl
305	4	8.2	115	5	US-09-739-449-11882	Sequence 11882, A	378	4	8.2	138	4	US-08-934-000-13	Sequence 13, Appl
306	4	8.2	115	5	US-09-380-910-3	Sequence 3, Appl	379	4	8.2	138	4	US-08-934-000-15	Sequence 15, Appl
307	4	8.2	116	1	PCT-US01-11988-544	Sequence 544, Ap	380	4	8.2	139	4	US-08-934-000-19	Sequence 19, Appl
308	4	8.2	116	5	US-09-833-245-544	Sequence 544, Ap	381	4	8.2	139	4	US-08-934-000-21	Sequence 21, Appl
309	4	8.2	116	5	US-09-155-739-41	Sequence 41, Appl	382	4	8.2	139	5	US-09-830-160-15	Sequence 15, Appl
310	4	8.2	117	5	US-09-380-910-5	Sequence 5, Appl	383	4	8.2	141	1	PCT-US01-01339-5220	Sequence 5220, Ap
311	4	8.2	118	1	PCT-US01-04098A-1307	Sequence 1307, Ap	384	4	8.2	141	1	PCT-US01-11663-408	Sequence 408, Ap
312	4	8.2	118	1	PCT-US00-35017A-938	Sequence 938, Ap	385	4	8.2	141	1	PCT-US01-01339-1950	Sequence 1950, Ap
313	4	8.2	118	5	US-09-739-449-12760	Sequence 12760, A	386	4	8.2	141	5	US-09-739-449-13274	Sequence 13274, A
314	4	8.2	119	1	PCT-US01-04098A-1623	Sequence 1623, Ap	387	4	8.2	142	1	PCT-US01-01350-87	Sequence 87, Appl
315	4	8.2	119	4	US-08-934-000-78	Sequence 78, Appl	388	4	8.2	142	1	PCT-US00-35017A-1292	Sequence 1292, Ap
316	4	8.2	119	4	US-08-934-000-79	Sequence 79, Appl	389	4	8.2	142	5	US-09-155-739-17	Sequence 17, Appl
317	4	8.2	119	4	US-08-934-000-80	Sequence 80, Appl	390	4	8.2	143	5	US-09-739-449-1748	Sequence 12748, A
318	4	8.2	119	4	US-08-934-000-81	Sequence 81, Appl	391	4	8.2	144	1	PCT-US01-11988-1592	Sequence 1592, Ap
319	4	8.2	119	5	US-09-155-739-10	Sequence 10, Appl	392	4	8.2	144	5	US-09-833-245-1592	Sequence 1592, Ap

393	4	8.2	145	1	PCT-US01-03782A-158	Sequence 158, App
394	4	8.2	145	5	US-09-640-211A-798	Sequence 798, App
395	4	8.2	147	5	PCT-US01-01339-3988	Sequence 3988, App
396	4	8.2	147	1	PCT-US01-01329-1409	Sequence 1409, App
397	4	8.2	147	5	US-09-739-449-9554	Sequence 9554, App
398	4	8.2	148	1	PCT-US01-01339-4077	Sequence 4077, App
399	4	8.2	148	1	PCT-US01-01329-1494	Sequence 1494, App
400	4	8.2	149	1	PCT-US01-01339-5278	Sequence 5278, App
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402	4	8.2	150	5	US-09-822-827-707	Sequence 707, App
403	4	8.2	151	1	PCT-US01-11663-404	Sequence 404, App
404	4	8.2	151	5	US-09-739-449-10411	Sequence 10411, A
405	4	8.2	155	1	PCT-US01-11988-1804	Sequence 1804, App
406	4	8.2	155	5	US-09-826-019-53	Sequence 53, Appl1
407	4	8.2	155	5	US-09-833-245-1804	Sequence 1804, App
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409	4	8.2	157	1	PCT-US01-01339-4578	Sequence 4578, App
410	4	8.2	157	1	PCT-US01-01329-1835	Sequence 1835, App
411	4	8.2	158	5	US-09-640-211A-2167	Sequence 2167, App
412	4	8.2	159	5	US-09-640-211A-818	Sequence 818, App
413	4	8.2	160	5	US-09-640-211A-699	Sequence 699, App
414	4	8.2	162	5	US-09-709-126-10	Sequence 10, Appl1
415	4	8.2	163	1	PCT-US00-35017A-751	Sequence 751, App
416	4	8.2	163	1	PCT-US01-01332-952	Sequence 952, App
417	4	8.2	164	5	US-09-739-449-12530	Sequence 12530, A
418	4	8.2	164	5	US-09-453-976-12	Sequence 12, Appl1
419	4	8.2	165	5	US-09-722-329-101	Sequence 101, App
420	4	8.2	167	1	PCT-US01-01339-3224	Sequence 3224, App
421	4	8.2	167	5	US-09-453-976-13	Sequence 13, Appl1
422	4	8.2	167	5	US-09-640-211A-838	Sequence 838, App
423	4	8.2	168	1	PCT-US01-01312-1019	Sequence 1019, App
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425	4	8.2	170	1	PCT-US01-01329-1206	Sequence 1206, App
426	4	8.2	171	5	US-09-739-449-11011	Sequence 11011, A
427	4	8.2	171	5	US-09-739-449-11614	Sequence 11614, A
428	4	8.2	171	6	US-60-248-505-877	Sequence 877, App
429	4	8.2	172	1	PCT-US00-35017A-1246	Sequence 1246, App
430	4	8.2	172	5	US-09-739-449-11002	Sequence 11002, A
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432	4	8.2	174	1	PCT-US00-35017A-1309	Sequence 1309, App
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434	4	8.2	175	5	US-09-739-449-11255	Sequence 11255, A
435	4	8.2	175	5	US-09-828-644-100	Sequence 100, App
436	4	8.2	175	5	US-09-640-211A-774	Sequence 774, App
437	4	8.2	175	6	US-60-248-505-1233	Sequence 1233, App
438	4	8.2	177	5	US-09-739-449-10719	Sequence 10719, A
439	4	8.2	178	6	US-60-248-505-1332	Sequence 1332, App
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443	4	8.2	181	1	PCT-US01-11988-910	Sequence 910, App
444	4	8.2	181	1	US-09-833-245-910	Sequence 910, App
445	4	8.2	182	1	PCT-US01-11988-1283	Sequence 1283, App
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447	4	8.2	182	5	US-09-833-245-1283	Sequence 1283, App
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449	4	8.2	184	1	PCT-US01-11988-1248	Sequence 1248, App
450	4	8.2	184	1	PCT-US01-11988-1249	Sequence 1249, App
451	4	8.2	184	5	US-09-739-449-8804	Sequence 8804, App
452	4	8.2	184	5	US-09-833-245-572	Sequence 572, App
453	4	8.2	184	5	US-09-833-245-1248	Sequence 1248, App
454	4	8.2	184	5	US-09-833-245-1249	Sequence 1249, App
455	4	8.2	187	5	US-09-739-449-12072	Sequence 12072, A
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457	4	8.2	188	1	PCT-US00-35017A-847	Sequence 847, App
458	4	8.2	188	5	US-09-463-891C-36	Sequence 36, Appl1
459	4	8.2	188	6	US-60-248-505-998	Sequence 998, App
460	4	8.2	189	1	PCT-US01-04098A-1330	Sequence 1330, App
461	4	8.2	189	5	US-09-821-803-4	Sequence 4, Appl1
462	4	8.2	189	5	US-09-828-644-114	Sequence 114, App
463	4	8.2	190	1	PCT-US00-30036A-92	Sequence 92, Appl1
464	4	8.2	190	1	PCT-US01-11988-692	Sequence 692, App
465	4	8.2	190	5	US-09-640-211A-766	Sequence 766, App
466	4	8.2	190	5	US-09-833-245-692	Sequence 692, App
467	4	8.2	193	5	US-09-739-449-10225	Sequence 10225, A
468	4	8.2	194	1	PCT-US01-01350-155	Sequence 155, App
469	4	8.2	195	1	PCT-US01-11988-610	Sequence 610, App
470	4	8.2	195	1	PCT-US00-35017A-1347	Sequence 1347, App
471	4	8.2	195	5	US-09-833-245-610	Sequence 610, App
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473	4	8.2	197	1	PCT-US01-04098A-3298	Sequence 3298, App
474	4	8.2	197	6	US-60-248-505-942	Sequence 942, App
475	4	8.2	198	1	PCT-US01-01339-3428	Sequence 3428, App
476	4	8.2	198	6	US-60-248-505-1158	Sequence 1158, App
477	4	8.2	200	1	PCT-US00-35017A-768	Sequence 768, App
478	4	8.2	202	1	PCT-US01-11988-1805	Sequence 1805, App
479	4	8.2	202	1	PCT-US01-01332-631	Sequence 631, App
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481	4	8.2	202	5	US-09-828-644-65	Sequence 65, Appl1
482	4	8.2	202	5	US-09-833-245-1805	Sequence 1805, App
483	4	8.2	203	5	US-09-193-562D-3	Sequence 3, Appl1
484	4	8.2	203	6	US-60-248-505-1246	Sequence 1246, App
485	4	8.2	204	1	PCT-US01-01332-725	Sequence 725, App
486	4	8.2	205	5	US-09-461-920B-3	Sequence 3, Appl1
487	4	8.2	206	5	US-09-828-644-116	Sequence 116, App
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490	4	8.2	208	6	US-60-248-505-1255	Sequence 1255, App
491	4	8.2	210	1	PCT-US00-35017A-802	Sequence 802, App
492	4	8.2	210	5	US-09-739-449-10470	Sequence 10470, A
493	4	8.2	210	5	US-09-811-284-429	Sequence 229, App
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497	4	8.2	212	5	US-09-640-211A-796	Sequence 796, App
498	4	8.2	213	1	PCT-US01-11988-1852	Sequence 1852, App
499	4	8.2	213	1	PCT-US01-04098A-1928	Sequence 1928, App
500	4	8.2	213	5	US-09-739-449-9632	Sequence 9632, App
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505	4	8.2	216	5	US-09-802-706-7	Sequence 7, Appl1
506	4	8.2	216	5	US-09-822-486-72	Sequence 22, Appl1
507	4	8.2	216	5	US-09-380-139A-59	Sequence 59, Appl1
508	4	8.2	217	1	PCT-US01-04098A-1748	Sequence 1748, App
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510	4	8.2	218	5	US-09-802-077-9	Sequence 9, Appl1
511	4	8.2	218	5	US-09-792-938-1	Sequence 1, Appl1
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513	4	8.2	219	1	PCT-US01-01332-1035	Sequence 1035, App
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516	4	8.2	221	1	PCT-US01-04098A-1731	Sequence 1731, App
517	4	8.2	221	1	PCT-US01-01332-766	Sequence 766, App
518	4	8.2	221	5	US-09-739-449-10626	Sequence 10626, A
519	4	8.2	221	5	US-09-828-644-71	Sequence 71, Appl1
520	4	8.2	223	1	PCT-US01-01310-63	Sequence 63, Appl1
521	4	8.2	223	6	US-60-248-505-807	Sequence 807, App
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523	4	8.2	224	1	PCT-US00-27237-140	Sequence 140, App
524	4	8.2	224	5	US-09-828-644-73	Sequence 73, Appl1
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526	4	8.2	225	1	PCT-US00-27237-162	Sequence 162, App
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534	4	8.2	228	5	US-09-821-225-2	Sequence 2, Appl1
535	4	8.2	229	1	PCT-US01-11988-1483	Sequence 1483, App
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542	4	8.2	229	5	US-09-833-245-1483	Sequence 1483, App	615	4	8.2	264	1	PCT-US01-04098A-3269	Sequence 3269, App
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550	4	8.2	234	1	PCT-US01-11988-2210	Sequence 2210, App	623	4	8.2	267	5	US-09-826-019-55	Sequence 55, App1
551	4	8.2	234	5	US-09-525-993-7	Sequence 7, App1	624	4	8.2	268	1	PCT-US01-04098A-1166	Sequence 1166, App
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553	4	8.2	234	5	US-09-833-245-1322	Sequence 1322, App	626	4	8.2	269	5	US-09-383-745-3	Sequence 3, App1
554	4	8.2	234	5	US-09-833-245-1803	Sequence 1803, App	627	4	8.2	270	5	US-09-739-449-10832	Sequence 10832, A
555	4	8.2	234	5	US-09-833-245-2210	Sequence 2210, App	628	4	8.2	270	5	US-09-821-803-6	Sequence 6, App1
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561	4	8.2	237	5	US-09-828-644-72	Sequence 72, App1	634	4	8.2	273	4	US-08-956-171C-5196	Sequence 5196, App
562	4	8.2	238	5	US-09-739-449-13258	Sequence 13258, A	635	4	8.2	273	5	US-09-739-449-9756	Sequence 9756, App
563	4	8.2	239	1	PCT-US01-01312-638	Sequence 638, App	636	4	8.2	273	5	US-09-739-449-9756	Sequence 9756, App
564	4	8.2	240	1	PCT-US01-04098A-1272	Sequence 1272, App	637	4	8.2	274	1	PCT-US01-01339-5338	Sequence 5338, App
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566	4	8.2	240	5	US-09-821-821-4	Sequence 4, App1	639	4	8.2	275	1	PCT-US01-04098A-3366	Sequence 3366, App
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569	4	8.2	242	1	PCT-US00-35017A-987	Sequence 987, App	642	4	8.2	277	5	US-09-739-449-10900	Sequence 10900, App
570	4	8.2	244	1	PCT-US01-11988-1060	Sequence 1060, App	643	4	8.2	277	5	US-09-336-910A-6	Sequence 6, App1
571	4	8.2	244	5	US-09-833-245-1060	Sequence 1060, App	644	4	8.2	278	5	US-09-810-264-28	Sequence 28, App1
572	4	8.2	247	5	US-09-832-129-57	Sequence 57, App1	645	4	8.2	280	1	US-09-792-024-100	Sequence 100, App
573	4	8.2	248	5	US-09-538-165A-4	Sequence 4, App1	646	4	8.2	280	1	PCT-US01-04098A-3041	Sequence 3041, App
574	4	8.2	249	1	PCT-US01-11988-335	Sequence 335, App	647	4	8.2	280	1	PCT-US01-04098A-3042	Sequence 3042, App
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576	4	8.2	249	5	US-09-833-245-335	Sequence 335, App	649	4	8.2	280	1	PCT-US01-01332-814	Sequence 814, App
577	4	8.2	250	5	US-09-739-449-8994	Sequence 8994, App	650	4	8.2	280	5	US-09-823-356-7	Sequence 7, App1
578	4	8.2	250	5	US-09-739-449-10671	Sequence 10671, App	651	4	8.2	282	1	PCT-US00-35017A-1392	Sequence 1392, App
579	4	8.2	251	4	US-08-956-171C-5252	Sequence 5252, App	652	4	8.2	282	1	PCT-US01-0112-782	Sequence 782, App
580	4	8.2	251	5	US-09-739-449-12852	Sequence 12852, A	653	4	8.2	282	5	US-09-739-449-12360	Sequence 12360, A
581	4	8.2	252	1	PCT-US01-11988-2226	Sequence 2226, App	654	4	8.2	284	6	US-60-248-505-06	Sequence 906, App
582	4	8.2	252	5	US-09-833-245-2226	Sequence 2226, App	655	4	8.2	285	5	US-09-739-449-10310	Sequence 10310, A
583	4	8.2	252	6	US-60-248-505-762	Sequence 762, App	656	4	8.2	286	1	PCT-US00-35017A-1425	Sequence 1425, App
584	4	8.2	253	5	US-09-823-494-20	Sequence 20, App1	657	4	8.2	288	1	PCT-US01-04098A-3783	Sequence 3783, App
585	4	8.2	253	6	US-60-248-505-880	Sequence 880, App	658	4	8.2	290	5	US-09-739-449-9480	Sequence 9480, App
586	4	8.2	254	5	US-09-739-449-11499	Sequence 11499, A	659	4	8.2	292	5	US-09-739-449-11557	Sequence 11557, A
587	4	8.2	254	5	US-09-823-494-19	Sequence 19, App1	660	4	8.2	293	5	US-09-739-449-11477	Sequence 11477, A
588	4	8.2	254	5	US-09-823-494-26	Sequence 26, App1	661	4	8.2	293	5	US-09-739-449-11851	Sequence 11851, A
589	4	8.2	254	5	US-09-823-494-28	Sequence 28, App1	662	4	8.2	294	1	PCT-US01-01332-680	Sequence 680, App
590	4	8.2	254	6	US-60-248-505-1033	Sequence 1033, App	663	4	8.2	294	1	PCT-US01-03401-12	Sequence 12, App1
591	4	8.2	255	5	US-09-739-449-12979	Sequence 12979, A	664	4	8.2	295	6	US-60-248-505-1321	Sequence 1321, App
592	4	8.2	255	5	US-09-640-211A-1163	Sequence 1163, App	665	4	8.2	295	5	US-09-739-449-10447	Sequence 10447, A
593	4	8.2	255	5	US-09-640-211A-2261	Sequence 2261, App	666	4	8.2	297	1	PCT-US01-0112-1162	Sequence 1162, App
594	4	8.2	256	1	PCT-US00-35017A-1077	Sequence 1077, App	667	4	8.2	297	5	US-09-739-449-8348	Sequence 8348, App
595	4	8.2	256	5	US-09-739-449-11977	Sequence 11977, A	668	4	8.2	297	5	US-09-097-221-10	Sequence 10, App1
596	4	8.2	256	5	US-09-823-494-22	Sequence 22, App1	669	4	8.2	297	5	US-60-248-505-733	Sequence 733, App
597	4	8.2	256	5	US-09-396-313A-67	Sequence 67, App1	670	4	8.2	298	6	US-09-739-449-9139	Sequence 9139, App
598	4	8.2	257	5	US-09-739-449-12260	Sequence 12260, A	671	4	8.2	298	5	US-09-739-449-12674	Sequence 12674, A
599	4	8.2	257	5	US-09-781-417-82	Sequence 82, App1	672	4	8.2	300	5	US-09-739-449-11319	Sequence 11319, A
600	4	8.2	258	5	US-09-739-449-13173	Sequence 13173, A	673	4	8.2	301	5	US-09-739-449-11943	Sequence 11943, A
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602	4	8.2	259	1	PCT-US00-35017A-1062	Sequence 1062, App	675	4	8.2	305	1	PCT-US01-09226-56	Sequence 56, App1
603	4	8.2	259	1	US-09-422-507A-2	Sequence 2, App1	676	4	8.2	305	5	PCT-US01-04098A-1285	Sequence 1285, App
604	4	8.2	260	1	PCT-US01-11988-1021	Sequence 1021, App	677	4	8.2	305	5	US-09-739-449-12821	Sequence 12821, A
605	4	8.2	260	5	US-09-739-449-10363	Sequence 10363, A	678	4	8.2	305	5	US-09-398-563A-2	Sequence 2, App1
606	4	8.2	260	5	US-09-739-449-12252	Sequence 12252, A	679	4	8.2	305	5	US-09-398-563A-4	Sequence 4, App1
607	4	8.2	260	5	US-09-833-245-1021	Sequence 1021, App	680	4	8.2	307	1	PCT-US01-01329-1586	Sequence 1586, App
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610	4	8.2	261	5	US-09-833-245-1020	Sequence 1020, App	683	4	8.2	308	1	PCT-US01-04098A-1042	Sequence 1042, App
611	4	8.2	263	5	US-09-740-288A-32	Sequence 32, App1	684	4	8.2	308	1	PCT-US01-04098A-3307	Sequence 3307, App

685	4	8.2	309	1	PCT-US01-01332-615	Sequence 615, App	758	4	8.2	348	1	PCT-US01-01332-1068	Sequence 1068, Ap
686	4	8.2	310	1	PCT-US01-04098A-3590	Sequence 3590, Ap	759	4	8.2	349	1	PCT-US01-04098A-3375	Sequence 3375, Ap
687	4	8.2	310	6	US-60-248-505-1265	Sequence 1265, Ap	760	4	8.2	349	1	PCT-US01-01332-956	Sequence 956, App
688	4	8.2	311	5	US-09-538-165A-3	Sequence 3, App11	761	4	8.2	349	1	PCT-US01-12306-5	Sequence 5, App11
689	4	8.2	312	5	US-09-549-066-55	Sequence 55, App1	762	4	8.2	349	5	US-09-343-011A-1	Sequence 1, App11
690	4	8.2	313	5	US-09-739-449-11729	Sequence 11729, A	763	4	8.2	349	5	US-09-826-509-503	Sequence 503, App
691	4	8.2	314	1	PCT-US01-11988-352	Sequence 592, App	764	4	8.2	350	1	PCT-US01-04098A-1738	Sequence 1738, Ap
692	4	8.2	314	5	US-09-739-449-8383	Sequence 8383, App	765	4	8.2	350	1	PCT-US01-01332-635	Sequence 635, App
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697	4	8.2	315	5	US-09-739-449-9594	Sequence 9594, App	770	4	8.2	353	1	PCT-US00-35017A-1297	Sequence 1297, Ap
698	4	8.2	315	5	US-09-151-771B-10	Sequence 10, App1	771	4	8.2	357	5	PCT-US01-10635-4	Sequence 4, App11
699	4	8.2	316	1	PCT-US01-11944-3	Sequence 3, App11	772	4	8.2	359	5	US-09-739-449-8493	Sequence 8493, Ap
700	4	8.2	316	4	US-08-956-171C-5231	Sequence 5231, Ap	773	4	8.2	360	5	US-09-739-449-12033	Sequence 12033, A
701	4	8.2	318	6	US-09-422-507A-4	Sequence 4, App1	774	4	8.2	360	5	US-09-669-476-2	Sequence 2, App11
702	4	8.2	320	1	US-60-248-505-1122	Sequence 1122, App	775	4	8.2	360	5	US-09-826-509-443	Sequence 443, App
703	4	8.2	320	1	PCT-US00-35017A-1149	Sequence 1149, Ap	776	4	8.2	362	5	US-09-739-449-8416	Sequence 8416, Ap
704	4	8.2	320	6	US-09-811-284-141	Sequence 141, App	777	4	8.2	363	1	PCT-US01-11988-2248	Sequence 2248, Ap
705	4	8.2	320	6	US-60-248-505-1059	Sequence 1059, Ap	778	4	8.2	363	1	PCT-US01-04098A-1030	Sequence 1030, Ap
706	4	8.2	322	5	US-09-806-258-1	Sequence 1, App11	779	4	8.2	363	5	US-09-792-024-80	Sequence 80, App1
707	4	8.2	322	5	US-09-806-258-6	Sequence 6, App11	780	4	8.2	363	5	US-09-832-129-34	Sequence 34, App1
708	4	8.2	323	1	PCT-US01-01339-3635	Sequence 3635, Ap	781	4	8.2	363	5	US-09-833-245-2248	Sequence 2248, Ap
709	4	8.2	323	1	PCT-US01-01329-1070	Sequence 1070, Ap	782	4	8.2	364	1	PCT-US01-04098A-1071	Sequence 1071, Ap
710	4	8.2	324	1	PCT-US01-01332-692	Sequence 692, App	783	4	8.2	364	4	US-08-706-945B-138	Sequence 138, App
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712	4	8.2	327	1	PCT-US01-04098A-3253	Sequence 3253, Ap	785	4	8.2	365	1	PCT-US00-35017A-901	Sequence 901, App
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ALIGNMENTS

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RESULT 1
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; GENERAL INFORMATION:
; APPLICANT: LI, Xiaomao
; APPLICANT: SAMBHARA, Suryaprakash
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: NUCLEIC ACID VACCINES ENCODING G PROTEIN OF RESPIRATORY
; FILE REFERENCE: 1038-1003 MIS:jb
; CURRENT APPLICATION NUMBER: US/09/462, 816
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: PCT/CA98/00697
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 08/896,442
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 232
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-09-462-816-4

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Query Match 81.6%; Score 40; DB 5; Length 232;
Best Local Similarity 100.0%; Pred. No. 8.6e-36;
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RESULT 2
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; APPLICANT: LI, Xiaomao
; APPLICANT: SAMBHARA, Suryaprakash
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: NUCLEIC ACID VACCINES ENCODING G PROTEIN OF RESPIRATORY
; FILE REFERENCE: 1038-1003 MIS:jb

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; CURRENT APPLICATION NUMBER: US/09/462, 816
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: PCT/CA98/00697
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 08/896,442
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 298
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-09-462-816-2

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Query Match 81.6%; Score 40; DB 5; Length 298;
Best Local Similarity 100.0%; Pred. No. 1e-35;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 10 KPNDHFVEVFNVPSCISNNPTCAICKRIPNKKPGKK 49
Db 158 KPNDHFVEVFNVPSCISNNPTCAICKRIPNKKPGKK 197

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RESULT 3
US-09-739-449-9007
; Sequence 9007, Application US/09739449
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15490)C
; CURRENT APPLICATION NUMBER: US/09/739,449
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/514,000
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 9007
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-09-739-449-9007

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Query Match 12.2%; Score 6; DB 5; Length 304;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 19 VFNVEVP 24
Db 215 VFNVEVP 220

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RESULT 4
US-09-739-449-8921
; Sequence 8921, Application US/09739449
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15490)C
; CURRENT APPLICATION NUMBER: US/09/739,449
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/514,000
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 8921
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-09-739-449-8921

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Query Match 12.2%; Score 6; DB 5; Length 405;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 VFNFPV 24
DB 268 VFNFPV 273

RESULT 5
US-09-654-289-9
; Sequence 9, Application US/09654289
; GENERAL INFORMATION:
; APPLICANT: Binz, Hans
; APPLICANT: N'Guyen, Ngoc Thien
; APPLICANT: Bausant, Thierry
; APPLICANT: Trudel, Michel
; TITLE OF INVENTION: PEPTIDE FRAGMENT OF RESPIRATORY
; TITLE OF INVENTION: SYNCYTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITION CONTAINING IT AND PREPARATION PROCESS
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Gordon W. Hueschen
; STREET: 715 The "H" Bldg., 310 East Michigan
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; ATTORNEY/AGENT INFORMATION:
; NAME: Hueschen, Gordon W.
; REGISTRATION NUMBER: 16,157
; REFERENCE/DOCKET NUMBER: PF57PCTUS/d1n
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616-382-2030
; TELEFAX: 616-382-2030
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: /product="Orn"
; ; OTHER INFORMATION: /note="sequence 174-187 / name : GI'A"
US-09-654-289-9

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Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 29 SNNPT 33
DB 4 SNNPT 8

RESULT 6
US-09-654-289-11
; Sequence 11, Application US/09654289
; GENERAL INFORMATION:
; APPLICANT: Binz, Hans
; APPLICANT: N'Guyen, Ngoc Thien
; APPLICANT: Bausant, Thierry
; APPLICANT: Trudel, Michel
; TITLE OF INVENTION: PEPTIDE FRAGMENT OF RESPIRATORY
; TITLE OF INVENTION: SYNCYTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITION CONTAINING IT AND PREPARATION PROCESS
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Gordon W. Hueschen
; STREET: 715 The "H" Bldg., 310 East Michigan
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; ATTORNEY/AGENT INFORMATION:
; NAME: Hueschen, Gordon W.
; REGISTRATION NUMBER: 16,157
; REFERENCE/DOCKET NUMBER: PF57PCTUS/d1n
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616-382-2030
; TELEFAX: 616-382-2030
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: /product="Orn"
; ; OTHER INFORMATION: /note="sequence 174-187 / name : GI'adeljac"
US-09-654-289-11

Query Match 10.2%; Score 5; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 29 SNNPT 33
DB 4 SNNPT 8

RESULT 7
US-09-654-289-19
; Sequence 19, Application US/09654289
; GENERAL INFORMATION:
; APPLICANT: Binz, Hans
; APPLICANT: N'Guyen, Ngoc Thien
; APPLICANT: Bausant, Thierry
; APPLICANT: Trudel, Michel
; TITLE OF INVENTION: PEPTIDE FRAGMENT OF RESPIRATORY

;; TITLE OF INVENTION: SYNCYTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICAL
;; TITLE OF INVENTION: COMPOSITION CONTAINING IT AND PREPARATION PROCESS
;; NUMBER OF SEQUENCES: 75
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Gordon W. Hueschen
;; STREET: 715 The "H" Bldg., 310 East Michigan
;; CITY: Kalamazoo
;; STATE: MI
;; COUNTRY: USA
;; ZIP: 49007
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
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;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/654,289
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/721,979
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hueschen, Gordon W.
;; REGISTRATION NUMBER: 16,157
;; REFERENCE/DOCKET NUMBER: PF57PCTUS/dln
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 616-382-0030
;; TELEFAX: 616-382-2030
;; INFORMATION FOR SEQ ID NO: 19:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 12
;; OTHER INFORMATION: /product="Orn"
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;; LOCATION: 16
;; OTHER INFORMATION: /product="Orn"
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;; OTHER INFORMATION: /note="sequence 171-187 / name : G4'A"
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;; US-09-654-289-19
;;
;; Query Match 10.2%; Score 5; DB 5; Length 17;
;; Best Local Similarity 100.0%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;;
QY 29 SNNPT 33
Db 7 SNNPT 11
;;
RESULT 8
US-09-654-289-20
;; Sequence 20, Application US/09654289
;; GENERAL INFORMATION:
;; APPLICANT: Binz, Hans
;; APPLICANT: N'Guyen, Ngoc Thien
;; APPLICANT: Baussant, Thierry
;; APPLICANT: Trudel, Michel
;; TITLE OF INVENTION: PEPTIDE FRAGMENT OF RESPIRATORY
;; TITLE OF INVENTION: SYNCYTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICAL
;; TITLE OF INVENTION: COMPOSITION CONTAINING IT AND PREPARATION PROCESS
;; NUMBER OF SEQUENCES: 75
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Gordon W. Hueschen

;; STREET: 715 The "H" Bldg., 310 East Michigan
;; CITY: Kalamazoo
;; STATE: MI
;; COUNTRY: USA
;; ZIP: 49007
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
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;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/654,289
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/721,979
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hueschen, Gordon W.
;; REGISTRATION NUMBER: 16,157
;; REFERENCE/DOCKET NUMBER: PF57PCTUS/dln
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 616-382-0030
;; TELEFAX: 616-382-2030
;; INFORMATION FOR SEQ ID NO: 20:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 12
;; OTHER INFORMATION: /product="Orn"
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;; OTHER INFORMATION: /note="sequence 171-187 / name : G4'AdeltaC"
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;; US-09-654-289-20
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;; Query Match 10.2%; Score 5; DB 5; Length 17;
;; Best Local Similarity 100.0%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;;
QY 29 SNNPT 33
Db 7 SNNPT 11
;;
RESULT 9
US-09-722-329-107
;; Sequence 107, Application US/09722329
;; GENERAL INFORMATION:
;; APPLICANT: Rosen et al.
;; TITLE OF INVENTION: 50 Human Secreted Proteins
;; FILE REFERENCE: P2016P1
;; CURRENT APPLICATION NUMBER: US/09/722,329
;; CURRENT FILING DATE: 2000-11-28
;; EARLIER APPLICATION NUMBER: 09/262,109
;; EARLIER FILING DATE: 1999-03-04
;; EARLIER APPLICATION NUMBER: 60/057,626
;; EARLIER FILING DATE: 1997-09-05
;; EARLIER APPLICATION NUMBER: 60/057,663
;; EARLIER FILING DATE: 1997-09-05
;; EARLIER APPLICATION NUMBER: 60/057,669
;; EARLIER FILING DATE: 1997-09-05
;; EARLIER APPLICATION NUMBER: 60/058,667
;; EARLIER FILING DATE: 1997-09-12
;; EARLIER APPLICATION NUMBER: 60/058,974
;; EARLIER FILING DATE: 1997-09-12
;; EARLIER APPLICATION NUMBER: 60/058,973
;; EARLIER FILING DATE: 1997-09-12

EARLIER APPLICATION NUMBER: 60/058,666
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/090,112
EARLIER FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 206
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 107
LENGTH: 26
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (26)
OTHER INFORMATION: Xaa equals stop translation
US-09-722-329-107

Query Match 10.2%; Score 5; DB 5; Length 26;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 26 SICSN 30
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Db 21 SICSN 25*

RESULT 10
PCT-US00-01979A-264
Sequence 264, Application PC/TUS0001979A
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Alpha-Conotoxin Peptides
FILE REFERENCE: Alphas 2
CURRENT APPLICATION NUMBER: PCT/US00/01979A
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/118,381
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 404
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 264
LENGTH: 36
TYPE: PRT
ORGANISM: Conus muscicus
PCT-US00-01979A-264

Query Match 10.2%; Score 5; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 30 NNPTC 34
|||||
Db 26 NNPTC 30

RESULT 11
US-09-493-795A-264
Sequence 264, Application US/09493795A
GENERAL INFORMATION:
APPLICANT: Watkins, Maren
APPLICANT: Olivera, Balomero M.
APPLICANT: Hillyard, David R.
APPLICANT: McIntosh, J. Michael
TITLE OF INVENTION: Alpha-Conotoxin Peptides
FILE REFERENCE: 2314-179.A
CURRENT APPLICATION NUMBER: US/09/493,795A
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/118,381
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 404
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 264
LENGTH: 36
TYPE: PRT
ORGANISM: Conus muscicus
US-09-493-795A-264

Query Match 10.2%; Score 5; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 30 NNPTC 34
|||||
Db 26 NNPTC 30

RESULT 12
PCT-US01-01321-1293
Sequence 1293, Application PC/TUS0101321
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc., et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC011PCT
CURRENT APPLICATION NUMBER: PCT/US01/01321
CURRENT FILING DATE: 2001-01-17
NUMBER OF SEQ ID NOS: 2181
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1293
LENGTH: 50
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (144)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (36)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PCT-US01-01321-1293

Query Match 10.2%; Score 5; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KORON 5
|||||
Db 39 KORON 43

RESULT 13
PCT-US01-01339-3605
Sequence 3605, Application PC/TUS0101339
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc., et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006PCT
CURRENT APPLICATION NUMBER: PCT/US01/01339
CURRENT FILING DATE: 2001-03-17
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3605
LENGTH: 52
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US01-01339-3605

Query Match 10.2%; Score 5; DB 1; Length 52;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 PPSKP 11

Db 37 ppskp 41

Search completed: May 21, 2001, 14:18:57
job time: 100 sec

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RESULT 14
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; Sequence 1416, Application PC/TUS0101321
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc., et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC011PCT
; CURRENT APPLICATION NUMBER: PCT/US01/01321
; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 2181
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1416
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (28)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
PCT-US01-01321-1416

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Query Match          10.2%; Score 5; DB 1; Length 55;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QRONK 6
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Db 1 QRONK 5

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RESULT 15
PCT-US01-01339-3043
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; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc., et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006PCT
; CURRENT APPLICATION NUMBER: PCT/US01/01339
; CURRENT FILING DATE: 2001-03-17
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3043
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (20)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (56)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (58)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
PCT-US01-01339-3043

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Query Match          10.2%; Score 5; DB 1; Length 74;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ppskp 11
   |||||
Db 22 ppskp 26

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 21, 2001, 14:16:16 ; Search time 18.73 Seconds
(without alignments)
149.546 Million cell updates/sec

Title: US-09-202-035-1

Perfect score: 49

Sequence: 1 KORQKPPSKPNNDHFHEVF.....NNPTCWAICKRIPNKKPGKK 49

Scoring table:

OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 390729 seqs, 57163235 residues

Word size : 0

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : A.Geneseq_0401.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	49	100.0	49	19	W39244 Human RSV G protei
3	49	100.0	49	19	W39248 Human RSV G protei
4	49	100.0	49	19	W39250 Human RSV G protei
5	49	100.0	49	19	W39251 Human RSV G protei
6	49	100.0	298	13	P70845 Sequence of human
7	49	100.0	298	13	R25302 HSRV glycoprotein
8	49	100.0	298	13	W47605 HSRV glycoprotein
9	49	100.0	681	10	P90441 Chimeric human res
10	48	98.0	49	19	W39219 Human RSV A subtyp
11	48	98.0	49	19	W39224 Human RSV A subtyp

12	46	93.9	49	19	W39220 Human RSV A subtyp
13	42	85.7	42	19	W39245 Human RSV G protei
14	40	81.6	43	20	W97304 Peptide which indu
15	40	81.6	49	19	W39218 Human RSV A subtyp
16	40	81.6	49	19	W39221 Human RSV A subtyp
17	40	81.6	49	19	W39222 Human RSV A subtyp
18	40	81.6	49	19	W39223 Human RSV A subtyp
19	40	81.6	59	17	R97073 Respiratory Syncyt
20	40	81.6	59	20	Y44100 RSV G protein anti
21	40	81.6	61	17	R97072 Respiratory Syncyt
22	40	81.6	61	20	Y44099 RSV G protein anti
23	40	81.6	101	16	R88253 RSV subgroup A wil
24	40	81.6	101	17	R95610 RSV sub-group A wi
25	40	81.6	101	17	R95616 Respiratory Syncyt
26	40	81.6	101	17	R97050 Respiratory Syncyt
27	40	81.6	101	20	Y44078 RSV G protein anti
28	40	81.6	101	21	B18805 A G2Na peptide der
29	40	81.6	232	20	W96314 Secreted G protein
30	40	81.6	298	14	R39286 Respiratory syncit
31	40	81.6	298	20	W96313 Membrane bound G p
32	40	81.6	349	17	R95660 Streptococcal prot
33	39	79.6	57	17	R97074 Respiratory Syncyt
34	39	79.6	57	20	Y44101 RSV G protein anti
35	37	75.5	55	17	R97075 Respiratory Syncyt
36	37	75.5	55	20	Y44102 RSV G protein anti
37	36	73.5	36	19	W39235 Human RSV G protei
38	36	73.5	36	19	W39236 Human RSV G protei
39	36	73.5	37	17	R88817 Respiratory syncyt
40	35	71.4	35	19	W39246 Human RSV G protei
41	35	71.4	35	19	W39249 Human RSV G protei
42	35	71.4	53	17	R97076 Respiratory Syncyt
43	35	71.4	53	20	Y44103 RSV G protein anti
44	34	69.4	101	20	W97311 Peptide which indu
45	33	67.3	33	17	R97078 Respiratory Syncyt
46	33	67.3	33	20	Y44105 RSV G protein anti
47	33	67.3	33	20	W97302 Peptide which indu
48	33	67.3	51	17	R97077 Respiratory Syncyt
49	33	67.3	51	20	Y44104 RSV G protein anti
50	33	67.3	101	20	W97310 Peptide which indu
51	32	65.3	32	17	R88813 Respiratory syncyt
52	29	59.2	29	19	W39247 Human RSV G protei
53	28	57.1	28	17	R88809 Respiratory syncyt
54	27	55.1	101	20	W97312 Peptide which indu
55	25	51.0	26	17	R87647 Synthetic RSV pept
56	22	44.9	23	17	R87648 Synthetic RSV pept
57	22	44.9	24	21	B15189 RSV G protein pept
58	21	42.9	24	21	Y95245 Respiratory syncyt
59	21	42.9	49	19	W39233 Human RSV G protei
60	19	38.8	19	19	W39237 Human RSV G protei
61	19	38.8	19	19	W39239 Human RSV G protei
62	19	38.8	19	19	W39240 Human RSV G protei
63	19	38.8	49	19	W39234 Human RSV G protei
64	17	34.7	17	17	R97064 Respiratory Syncyt
65	17	34.7	17	20	Y44091 RSV G protein anti
66	17	34.7	17	20	W93552 RSV attachment G p
67	17	34.7	17	20	W97315 Peptide which indu
68	16	32.7	16	20	W93549 RSV attachment G p
69	16	32.7	16	20	W93550 RSV attachment G p
70	15	30.6	15	19	W39238 Human RSV G protei
71	15	30.6	15	19	W39242 Human RSV G protei
72	15	30.6	15	19	W39243 Human RSV G protei
73	15	30.6	15	20	Y29703 Respiratory syncyt
74	15	30.6	15	20	W93553 RSV attachment G p
75	15	30.6	33	17	R97085 Respiratory Syncyt
76	15	30.6	33	20	Y44112 RSV G protein anti
77	15	30.6	51	17	R97084 Respiratory Syncyt
78	15	30.6	51	20	Y44111 RSV G protein anti
79	15	30.6	53	17	R97083 Respiratory Syncyt
80	15	30.6	53	20	Y44110 RSV G protein anti
81	15	30.6	55	17	R97082 Respiratory Syncyt
82	15	30.6	55	20	Y44109 RSV G protein anti
83	15	30.6	57	17	R97081 Respiratory Syncyt
84	15	30.6	57	20	Y44108 RSV G protein anti

85	15	30.6	59	17	R97080	Respiratory Syncyt	158	9	18.4	59	20	Y44121	RSV G protein anti
86	15	30.6	59	20	Y44107	Respiratory Syncyt	159	9	18.4	61	17	R97093	Respiratory Syncyt
87	15	30.6	61	17	R97079	Respiratory Syncyt	160	9	18.4	61	20	Y44120	RSV G protein anti
88	15	30.6	61	20	Y44106	RSV G protein anti	161	9	18.4	101	16	R88256	RSV subgroup B mod
89	15	30.6	101	16	R88235	RSV subgroup A mod	162	9	18.4	101	17	R95613	RSV subgp. B prote
90	15	30.6	101	17	R95612	RSV subgp. A prote	163	9	18.4	101	17	R95619	RSV sub-group B mu
91	15	30.6	101	17	R95618	Respiratory Syncyt	164	9	18.4	101	17	R97053	Respiratory Syncyt
92	15	30.6	101	17	R97052	Respiratory Syncyt	165	9	18.4	101	20	Y44081	RSV G protein anti
93	15	30.6	101	17	Y44080	RSV G protein anti	166	8	18.3	15	20	R97306	Peptide which indu
94	15	30.6	356	17	R95661	Immunogenic carrie	167	8	18.3	16	17	R97082	Respiratory Syncyt
95	14	28.6	14	16	R88245	Respiratory syncyt	168	8	18.3	16	20	R97300	Peptide which indu
96	14	28.6	14	17	R97054	Respiratory Syncyt	169	8	18.3	28	17	R95620	RSV sub-group B mu
97	14	28.6	14	20	Y44082	RSV G protein anti	170	7	14.3	244	13	R20929	Envelope proteins
98	14	28.6	14	20	W93551	RSV attachment G p	171	6	12.2	15	20	W93555	RSV attachment G p
99	14	28.6	15	20	W93554	Peptide which indu	172	6	12.2	17	17	R97086	Respiratory Syncyt
100	13	26.5	33	20	R97308	Peptide which indu	173	6	12.2	17	20	Y44093	RSV G protein anti
101	13	26.5	28	17	R88808	Respiratory syncyt	174	6	12.2	17	20	R97316	Peptide having int
102	13	26.5	32	17	R88812	Respiratory syncyt	175	6	12.2	28	15	R65761	Human 28-mer pepti
103	13	26.5	33	17	R97092	Respiratory Syncyt	176	6	12.2	28	15	R65762	Human cancer assoc
104	13	26.5	33	20	Y44119	RSV G protein anti	177	6	12.2	75	21	B43901	Arabidopsis thalia
105	13	26.5	33	20	W97303	Peptide which indu	178	6	12.2	76	21	G57267	Arabidopsis thalia
106	13	26.5	37	17	R88816	Respiratory syncyt	179	6	12.2	128	21	G09850	Arabidopsis thalia
107	13	26.5	43	20	W97305	Peptide which indu	180	6	12.2	138	21	G09849	Arabidopsis thalia
108	13	26.5	49	19	W39225	Human RSV B subtyp	181	6	12.2	188	10	P93469	Sequence encoded b
109	13	26.5	49	19	W39226	Human RSV B subtyp	182	6	12.2	222	21	G36194	Arabidopsis thalia
110	13	26.5	49	19	W39227	Human RSV B subtyp	183	6	12.2	227	21	G14146	Arabidopsis thalia
111	13	26.5	49	19	W39228	Human RSV B subtyp	184	6	12.2	227	21	G43029	Arabidopsis thalia
112	13	26.5	49	19	W39229	Human RSV B subtyp	185	6	12.2	243	21	G14145	Arabidopsis thalia
113	13	26.5	49	19	W39230	Human RSV B subtyp	186	6	12.2	243	21	G43028	Arabidopsis thalia
114	13	26.5	49	19	W39231	Human RSV B subtyp	187	6	12.2	243	21	G51627	Arabidopsis thalia
115	13	26.5	51	17	R97091	Respiratory Syncyt	188	6	12.2	246	21	G36193	Arabidopsis thalia
116	13	26.5	51	20	Y44118	RSV G protein anti	189	6	12.2	246	21	G14144	Arabidopsis thalia
117	13	26.5	53	20	R97090	Respiratory Syncyt	190	6	12.2	246	21	G43027	Arabidopsis thalia
118	13	26.5	53	20	Y44117	RSV G protein anti	191	6	12.2	246	21	G51626	Arabidopsis thalia
119	13	26.5	55	17	R97089	Respiratory Syncyt	192	6	12.2	299	21	G51625	Arabidopsis thalia
120	13	26.5	55	20	Y44116	RSV G protein anti	193	6	12.2	337	20	Y00281	Human secreted pro
121	13	26.5	57	17	R97088	Respiratory Syncyt	194	6	12.2	359	21	G36192	Arabidopsis thalia
122	13	26.5	57	20	Y44115	RSV G protein anti	195	6	12.2	397	21	G31564	Arabidopsis thalia
123	13	26.5	59	17	R97087	Respiratory Syncyt	196	6	12.2	402	21	G31563	Arabidopsis thalia
124	13	26.5	59	20	Y44114	RSV G protein anti	197	6	12.2	402	21	G38778	Arabidopsis thalia
125	13	26.5	61	17	R97086	Respiratory Syncyt	198	6	12.2	409	8	P70284	Protein A - beta-g
126	13	26.5	61	20	Y44113	RSV G protein anti	199	6	12.2	411	21	G38777	Arabidopsis thalia
127	13	26.5	101	16	R88254	RSV subgroup B wi	200	6	12.2	412	20	Y59733	Human normal ovari
128	13	26.5	101	17	R95611	RSV subgp. B prote	201	6	12.2	415	21	G38776	Arabidopsis thalia
129	13	26.5	101	17	R95617	RSV sub-group B wi	202	6	12.2	416	21	G31562	Arabidopsis thalia
130	13	26.5	101	17	R97051	Respiratory Syncyt	203	6	12.2	421	8	P70283	Protein A - beta-g
131	13	26.5	101	20	Y44079	RSV G protein anti	204	6	12.2	483	5	P40694	Sequence encoded b
132	12	24.5	14	16	R88247	Respiratory Syncyt	205	6	12.2	483	5	P40181	Sequence encoded b
133	12	24.5	14	17	R97056	Respiratory Syncyt	206	6	12.2	508	13	R23850	Vasoactive intesti
134	12	24.5	14	20	Y44084	RSV G protein anti	207	6	12.2	516	5	P40135	Sequence of protei
135	12	24.5	14	20	Y01503	Peptide which indu	208	6	12.2	516	8	P70282	Protein A - beta-q
136	12	24.5	16	13	R28758	Glycoprotein G epi	209	6	12.2	585	8	P70282	Arabidopsis thalia
137	12	24.5	17	17	R97065	Respiratory Syncyt	210	6	12.2	1249	21	G50830	Arabidopsis thalia
138	12	24.5	17	20	Y44092	RSV G protein anti	211	6	12.2	1254	21	G50829	Arabidopsis thalia
139	12	24.5	30	17	R95621	RSV sub-group A mu	212	5	10.2	1268	21	G50828	Arabidopsis thalia
140	12	24.5	92	17	R95615	RSV subgp. A prote	213	5	10.2	9	16	R85720	Template peptide f
141	12	24.5	101	17	R95614	RSV subgp. A prote	214	5	10.2	11	21	B15265	Specific factor VI
142	12	24.5	101	17	R97063	Respiratory Syncyt	215	5	10.2	12	17	W05294	Template backbone
143	12	24.5	101	20	Y44090	RSV G protein anti	216	5	10.2	13	19	W70131	Peptide produced b
144	10	20.4	10	19	W39241	Human RSV G protei	217	5	10.2	14	16	R88249	Respiratory syncyt
145	10	20.4	15	20	W93548	Peptide which indu	218	5	10.2	14	16	R88251	Respiratory syncyt
146	9	18.4	13	20	W97309	Peptide which indu	219	5	10.2	14	17	R97058	Respiratory Syncyt
147	9	18.4	33	17	R97099	Respiratory Syncyt	220	5	10.2	14	17	R97060	Respiratory Syncyt
148	9	18.4	33	20	Y44126	RSV G protein anti	221	5	10.2	14	20	Y44086	RSV G protein anti
149	9	18.4	51	17	R97098	Respiratory Syncyt	222	5	10.2	14	20	Y44088	RSV G protein anti
150	9	18.4	51	20	Y44125	Respiratory Syncyt	223	5	10.2	14	20	W93567	RSV attachment G p
151	9	18.4	53	17	R97097	Respiratory Syncyt	224	5	10.2	14	20	W97298	Peptide produced b
152	9	18.4	53	20	Y44124	RSV G protein anti	225	5	10.2	15	19	W70149	Peptide produced b
153	9	18.4	55	17	R97096	Respiratory Syncyt	226	5	10.2	17	17	R97068	Respiratory Syncyt
154	9	18.4	55	20	Y44123	RSV G protein anti	227	5	10.2	17	17	R97069	Respiratory Syncyt
155	9	18.4	57	17	R97095	Respiratory Syncyt	228	5	10.2	17	20	Y44095	RSV G protein anti
156	9	18.4	57	20	Y44122	RSV G protein anti	229	5	10.2	17	20	Y44096	RSV G protein anti
157	9	18.4	59	17	R97094	Respiratory Syncyt	230	5	10.2	18	14	R41939	Systemin. Lycoper
							230	5	10.2	18	20	W99102	Tomato systemin.

231	5	10.2	18	20	W97629	Tomato peptide hor	304	5	10.2	136	21	B54155	Human pancreatic c
232	5	10.2	18	21	B30686	Amino acid sequenc	305	5	10.2	138	21	B42439	Human ORFX ORF2203
233	5	10.2	19	21	W17416	Chicken anaemia vi	306	5	10.2	138	21	B08117	A polyphenol oxida
234	5	10.2	21	18	W14156	Human A33 antigen	307	5	10.2	139	18	W32903	Rat neurotrophic f
235	5	10.2	23	20	W86747	Anticoagulant pept	308	5	10.2	141	21	G27689	Arabidopsis thalia
236	5	10.2	23	20	W86748	Anticoagulant pept	309	5	10.2	141	21	G35313	Zea mays protein f
237	5	10.2	23	20	W86749	Anticoagulant pept	310	5	10.2	141	21	G57150	Arabidopsis thalia
238	5	10.2	23	20	W86745	Anticoagulant pept	311	5	10.2	142	21	B25507	Eucalyptus grandis
239	5	10.2	26	20	Y12955	Amino acid sequenc	312	5	10.2	143	21	G05220	Arabidopsis thalia
240	5	10.2	32	17	W02228	CD16:5:zeta(48-65)	313	5	10.2	143	21	G37407	Arabidopsis thalia
241	5	10.2	32	17	R89463	CD16:5:zeta(48-65)	314	5	10.2	145	18	W20455	H. pylori cytoplas
242	5	10.2	36	21	B21568	Cone snail alpha-c	315	5	10.2	145	18	W24664	H. pylori cytoplas
243	5	10.2	42	19	Y21513	Human neuroendocri	316	5	10.2	146	21	Y55838	Mouse SPOR01 poly
244	5	10.2	43	20	Y25813	Human secreted pro	317	5	10.2	147	20	Y29506	Human lung tumour
245	5	10.2	46	20	Y30875	Human secreted pro	318	5	10.2	147	21	B44445	Human lung tumour
246	5	10.2	47	21	B39022	Human secreted pro	319	5	10.2	148	21	G05046	Arabidopsis thalia
247	5	10.2	51	21	G09763	Arabidopsis thalia	320	5	10.2	148	21	G26877	Zea mays protein f
248	5	10.2	64	20	Y38401	Human secreted pro	321	5	10.2	152	21	G26876	Zea mays protein f
249	5	10.2	64	21	G33287	Zea mays protein f	322	5	10.2	152	21	B27614	Human secreted pro
250	5	10.2	67	21	B25316	Eucalyptus grandis	323	5	10.2	153	21	G12403	Zea mays protein f
251	5	10.2	68	21	B27618	Human secreted pro	324	5	10.2	154	21	G09456	Arabidopsis thalia
252	5	10.2	68	21	Y32145	Human secreted pro	325	5	10.2	157	21	Y81594	Streptococcus pneu
253	5	10.2	69	21	B12941	Neurotransmission	326	5	10.2	158	21	G54449	Zea mays protein f
254	5	10.2	72	20	Y04915	Mycobacterium spec	327	5	10.2	159	20	Y29505	Human lung tumour
255	5	10.2	73	21	Y69027	Amino acid sequenc	328	5	10.2	159	21	B44444	Human lung tumour
256	5	10.2	77	18	W20189	H. pylori cytoplas	329	5	10.2	159	21	G40887	Zea mays protein f
257	5	10.2	79	21	G33475	Arabidopsis thalia	330	5	10.2	161	18	W11587	Human breast cance
258	5	10.2	84	22	B65013	Human secreted pro	331	5	10.2	161	20	W88052	Protein encoded by
259	5	10.2	86	13	R20695	Modified human pro	332	5	10.2	161	21	Y81899	Fragment of gp30/a
260	5	10.2	86	13	R20693	Modified human pro	333	5	10.2	162	20	Y18128	Clone 2 of A. thal
261	5	10.2	86	13	R20694	Modified human pro	334	5	10.2	162	20	R68567	Human NDF-beta3 cl
262	5	10.2	90	21	B25124	Eucalyptus grandis	335	5	10.2	163	16	W15254	Human FC99 phospho
263	5	10.2	93	21	B44361	Human secreted pro	336	5	10.2	164	18	W15258	Rat FC99 phosphory
264	5	10.2	96	16	R70799	Human secreted pro	337	5	10.2	164	18	G27688	Arabidopsis thalia
265	5	10.2	96	21	B15805	Human chemokine I-	338	5	10.2	164	21	G54623	Zea mays protein f
266	5	10.2	98	21	G35451	Zea mays protein f	339	5	10.2	164	21	G57149	Arabidopsis thalia
267	5	10.2	99	21	G40827	Zea mays protein f	340	5	10.2	165	15	R51719	Partial sequence o
268	5	10.2	100	15	R51722	Partial sequence o	341	5	10.2	165	18	W32902	Rat neurotrophic f
269	5	10.2	100	21	B38309	Human secreted pro	342	5	10.2	165	21	G24740	Arabidopsis thalia
270	5	10.2	101	21	B53234	Human colon cancer	343	5	10.2	167	21	B53528	Human colon cancer
271	5	10.2	105	21	G56157	Arabidopsis thalia	344	5	10.2	168	21	G37406	Arabidopsis thalia
272	5	10.2	106	14	R41358	P. yoelii combined	345	5	10.2	168	21	G39345	Arabidopsis thalia
273	5	10.2	106	20	Y55723	FKHL7 forkhead dom	346	5	10.2	169	21	G54748	Arabidopsis thalia
274	5	10.2	106	20	Y55724	FKHL14 forkhead do	347	5	10.2	170	20	Y29215	Amino acid sequenc
275	5	10.2	107	21	G17879	Arabidopsis thalia	348	5	10.2	173	21	B25258	Eucalyptus grandis
276	5	10.2	107	21	G50035	Arabidopsis thalia	349	5	10.2	179	21	G36936	Arabidopsis thalia
277	5	10.2	107	21	G56156	Arabidopsis thalia	350	5	10.2	184	21	G05045	Arabidopsis thalia
278	5	10.2	108	21	G41963	Arabidopsis thalia	351	5	10.2	184	21	G08592	Arabidopsis thalia
279	5	10.2	109	15	R51721	Partial sequence o	352	5	10.2	184	21	G24739	Arabidopsis thalia
280	5	10.2	115	18	W28027	Amino acid sequenc	353	5	10.2	187	21	G40886	Zea mays protein f
281	5	10.2	115	21	G35314	Zea mays protein f	354	5	10.2	188	21	G08591	Arabidopsis thalia
282	5	10.2	116	21	G41962	Arabidopsis thalia	355	5	10.2	190	21	G29127	Arabidopsis thalia
283	5	10.2	120	21	B52089	Gene 38 human secr	356	5	10.2	190	21	G38040	Arabidopsis thalia
284	5	10.2	120	21	B52090	Human secreted pro	357	5	10.2	191	15	R54217	L.lactis branched
285	5	10.2	120	21	B21028	Human nucleic acid	358	5	10.2	194	21	G23431	Arabidopsis thalia
286	5	10.2	120	21	G56155	Arabidopsis thalia	359	5	10.2	195	21	B42025	Human ORFX ORF1789
287	5	10.2	121	16	R65201	VP3 protein, Chic	360	5	10.2	196	21	B42596	Human ORFX ORF2360
288	5	10.2	121	17	R88499	VP3 of chicken inf	361	5	10.2	197	21	G58186	Arabidopsis thalia
289	5	10.2	122	18	W32904	Rat neurotrophic f	362	5	10.2	200	14	R41938	Prosystemin, Lyco
290	5	10.2	122	21	G17426	Arabidopsis thalia	363	5	10.2	200	20	W99101	Tomato prosystemin
291	5	10.2	124	21	G17878	Arabidopsis thalia	364	5	10.2	200	20	W97625	Tomato prosystemin
292	5	10.2	124	21	G50034	Arabidopsis thalia	365	5	10.2	200	21	B30680	Amino acid sequenc
293	5	10.2	126	18	W16453	E. coli acyl carri	366	5	10.2	200	21	Y68979	Cps9F protein whic
294	5	10.2	127	18	W21854	Humanised light ch	367	5	10.2	202	16	R77524	NK-lysin full len
295	5	10.2	127	18	W21855	Humanised light ch	368	5	10.2	203	21	G08590	Arabidopsis thalia
296	5	10.2	128	21	B34068	Human secreted pro	369	5	10.2	205	20	W74465	F11 antigen protei
297	5	10.2	130	21	B40509	Human ORFX ORF273	370	5	10.2	205	21	B56481	Human prostate can
298	5	10.2	131	21	B58736	Breast and ovarian	371	5	10.2	205	21	Y74742	Weissneria meningit
299	5	10.2	131	21	G54450	Zea mays protein f	372	5	10.2	209	21	G29126	Arabidopsis thalia
300	5	10.2	132	21	B25142	Pinus radiata cell	373	5	10.2	209	21	G38039	Arabidopsis thalia
301	5	10.2	135	21	G27690	Arabidopsis thalia	374	5	10.2	210	21	G13888	Arabidopsis thalia
302	5	10.2	135	21	G54624	Zea mays protein f	375	5	10.2	210	21	G20761	Arabidopsis thalia
303	5	10.2	135	21	G57151	Arabidopsis thalia	376	5	10.2	210	21	G45185	Arabidopsis thalia

377	5	10.2	210	21	G45196	Arabidopsis thalia	450	5	10.2	273	20	Y08075	Human A33 protein
378	5	10.2	213	19	B19171	Amino acid sequenc	451	5	10.2	273	20	Y23329	An A33 related ant
379	5	10.2	214	19	G85808	S. pneumoniae deri	452	5	10.2	273	21	G08347	Arabidopsis thalia
380	5	10.2	217	20	W88104	A Rab protein desi	453	5	10.2	273	21	G32582	Arabidopsis thalia
381	5	10.2	217	21	G24738	Arabidopsis thalia	454	5	10.2	273	21	G51392	Arabidopsis thalia
382	5	10.2	219	21	G16787	Arabidopsis thalia	455	5	10.2	274	21	G13887	Arabidopsis thalia
383	5	10.2	219	21	Y76981	Quail H1 histone p	456	5	10.2	274	21	G20760	Arabidopsis thalia
384	5	10.2	220	14	R39700	Peptide sequence h	457	5	10.2	274	21	G39344	Arabidopsis thalia
385	5	10.2	220	16	R00553	S-SPV-001 potentia	458	5	10.2	274	21	G45184	Arabidopsis thalia
386	5	10.2	220	19	Y11027	H. pylori ORF 02ge	459	5	10.2	274	21	G45195	Arabidopsis thalia
387	5	10.2	220	20	Y17195	H. pylori outer me	460	5	10.2	275	21	G09455	Arabidopsis thalia
388	5	10.2	221	19	W80645	S. pneumoniae prot	461	5	10.2	276	20	Y34505	Porphyromonas ging
389	5	10.2	221	21	G05416	Arabidopsis thalia	462	5	10.2	280	20	Y34378	Porphyromonas ging
390	5	10.2	221	21	Y74740	Neisseria gonorrhoe	463	5	10.2	280	21	G39253	Gene 15 human secr
391	5	10.2	224	12	R11494	Endothelin-3 precu	464	5	10.2	284	21	G39783	Arabidopsis thalia
392	5	10.2	224	13	R25159	Endothelin-3 precu	465	5	10.2	285	21	G04683	Arabidopsis thalia
393	5	10.2	224	21	G21905	Arabidopsis thalia	466	5	10.2	285	21	G21575	Arabidopsis thalia
394	5	10.2	225	21	G05445	Arabidopsis thalia	467	5	10.2	285	21	G53563	Arabidopsis thalia
395	5	10.2	226	14	R38875	Sequence of haemag	468	5	10.2	286	17	W03566	Mycobacterium tube
396	5	10.2	226	15	R60213	Immunogenic fragme	469	5	10.2	286	20	Y19836	B. burgdorferi ant
397	5	10.2	226	17	W09318	Human wild type ch	470	5	10.2	290	21	B54365	Human pancreatic c
398	5	10.2	226	17	W09319	Human chymase clon	471	5	10.2	290	21	G21313	Arabidopsis thalia
399	5	10.2	226	17	W09320	Human chymase clon	472	5	10.2	291	21	G54148	Arabidopsis thalia
400	5	10.2	226	19	Y85978	S. pneumoniae deri	473	5	10.2	292	21	G04662	Arabidopsis thalia
401	5	10.2	228	21	G58185	Arabidopsis thalia	474	5	10.2	292	21	G53562	Arabidopsis thalia
402	5	10.2	229	17	R95274	Nisin nlsR gene pr	475	5	10.2	292	16	R68575	Arabidopsis thalia
403	5	10.2	229	21	G17425	Arabidopsis thalia	476	5	10.2	298	19	W61379	Rat NDF encoded by
404	5	10.2	230	21	G11474	Arabidopsis thalia	477	5	10.2	298	16	Y08071	Human junctional a
405	5	10.2	231	16	R68570	Rat NDF encoded by	478	5	10.2	299	20	Y23321	Human PRO307 prote
406	5	10.2	231	22	R36603	Human FLEXHR-25 pr	479	5	10.2	299	20	Y13364	Amino acid sequenc
407	5	10.2	233	21	G11473	Arabidopsis thalia	480	5	10.2	299	20	W74405	Amino acid sequenc
408	5	10.2	236	20	Y09153	Human CD81m protei	481	5	10.2	299	21	B24405	F11 antigen protei
409	5	10.2	238	13	R23785	Prepro ET-3 sequen	482	5	10.2	299	21	G36935	Human PRO301 prote
410	5	10.2	239	21	B43632	Human cancer assoc	483	5	10.2	299	21	Y95344	Arabidopsis thalia
411	5	10.2	239	21	G07529	Arabidopsis thalia	484	5	10.2	299	21	Y70670	Human PRO301 antit
412	5	10.2	239	21	G11472	Arabidopsis thalia	485	5	10.2	299	21	Y76011	Human A33 receptor
413	5	10.2	240	13	R20928	Envelope proteins	486	5	10.2	299	21	Y76076	Human A33 receptor
414	5	10.2	241	13	R29574	Human heregulin-be	487	5	10.2	299	22	B55950	Skin cell protein,
415	5	10.2	241	17	R27468	Glial growth facto	488	5	10.2	299	22	B56015	Skin cell protein,
416	5	10.2	241	20	Y06637	Herugelin-beta-3.	489	5	10.2	299	22	B53086	Human angiogenesis
417	5	10.2	241	21	Y71174	Human Heregulin HR	490	5	10.2	300	15	R56481	CD38. Homo sapien
418	5	10.2	242	21	G17424	Arabidopsis thalia	491	5	10.2	300	19	W61380	Mouse junctional a
419	5	10.2	245	21	G36996	Arabidopsis thalia	492	5	10.2	300	19	W3928	Amino acid sequenc
420	5	10.2	245	21	G53882	Arabidopsis thalia	493	5	10.2	300	20	Y23325	A33 related antige
421	5	10.2	246	18	W20840	H. pylori cytoplas	494	5	10.2	300	21	G16786	Arabidopsis thalia
422	5	10.2	246	21	B58196	Lung cancer associ	495	5	10.2	305	21	Y97042	B. subtilis oppc m
423	5	10.2	247	20	W73878	Human chymase prot	496	5	10.2	305	21	G04661	Arabidopsis thalia
424	5	10.2	247	21	B42519	Human ORFX ORF2283	497	5	10.2	305	21	G53561	Arabidopsis thalia
425	5	10.2	248	17	R88712	Tunicate serine pr	498	5	10.2	306	21	G16785	Arabidopsis thalia
426	5	10.2	248	20	Y39924	Bovine rotavirus W	499	5	10.2	317	20	Y19969	B. burgdorferi ant
427	5	10.2	248	21	Y77988	Human MBP amino ac	500	5	10.2	317	21	G37740	Arabidopsis thalia
428	5	10.2	251	19	W53008	Mus musculus I-mfb	501	5	10.2	318	18	W14158	Mouse A33 antigen.
429	5	10.2	255	21	C58184	Arabidopsis thalia	502	5	10.2	318	20	Y74150	Human prostate tum
430	5	10.2	257	21	G07568	Arabidopsis thalia	503	5	10.2	318	21	G07743	Arabidopsis thalia
431	5	10.2	257	21	G17567	Arabidopsis thalia	504	5	10.2	318	21	G08190	Arabidopsis thalia
432	5	10.2	257	21	G52536	Arabidopsis thalia	505	5	10.2	319	18	W14146	Human A33 antigen.
433	5	10.2	258	21	G21577	Arabidopsis thalia	506	5	10.2	319	20	Y23323	Amino acid sequenc
434	5	10.2	258	21	G39785	Arabidopsis thalia	507	5	10.2	319	22	B65863	Human A33 protein
435	5	10.2	259	21	G36995	Arabidopsis thalia	508	5	10.2	320	22	B60094	Human transport pr
436	5	10.2	259	21	G53881	Arabidopsis thalia	509	5	10.2	323	21	G36934	Arabidopsis thalia
437	5	10.2	260	20	Y08072	Human DNA40628 pro	510	5	10.2	324	17	R88558	V.harveyi lucifera
438	5	10.2	260	20	Y23326	An A33 related ant	511	5	10.2	325	17	W03565	Mycobacterium tube
439	5	10.2	261	12	R13505	P.denitrificans CO	512	5	10.2	325	21	B51703	Gene 34 human secr
440	5	10.2	262	21	G37741	Arabidopsis thalia	513	5	10.2	325	21	Y97281	Fibronectin attach
441	5	10.2	262	21	G45775	Arabidopsis thalia	514	5	10.2	326	21	G06827	Arabidopsis thalia
442	5	10.2	263	20	Y08074	Human DNA40628 pro	515	5	10.2	326	21	G49383	Arabidopsis thalia
443	5	10.2	263	20	Y23328	An A33 related ant	516	5	10.2	327	21	Y74737	Neisseria gonorrhoe
444	5	10.2	268	20	Y08073	Human A33 protein.	517	5	10.2	327	21	B39359	Human secreted pro
445	5	10.2	270	20	Y23327	An A33 related ant	518	5	10.2	329	21	G54896	Arabidopsis thalia
446	5	10.2	270	20	Y19837	B. burgdorferi ant	519	5	10.2	329	21	G39343	Arabidopsis thalia
447	5	10.2	270	21	G21576	Arabidopsis thalia	520	5	10.2	330	16	R79967	Fifth transmembran
448	5	10.2	270	21	G39784	Arabidopsis thalia	521	5	10.2	332	18	W32418	Mycobacterium tube
449	5	10.2	272	21	B54235	Human pancreatic c	522	5	10.2	332	18	W32350	Mycobacterium tube

523	5	10.2	332	19	W81683	M. tuberculosis im	596	5	10.2	404	21	G45866	Arabidopsis thalia
524	5	10.2	332	19	W64322	Mycobacterium tube	597	5	10.2	406	20	Y49152	Amino acid sequenc
525	5	10.2	332	20	Y39083	M. tuberculosis an	598	5	10.2	409	21	G59031	Arabidopsis thalia
526	5	10.2	332	20	Y38945	M. tuberculosis re	599	5	10.2	410	19	W77354	Human telomere rep
527	5	10.2	332	21	G36394	Arabidopsis thalia	600	5	10.2	412	20	Y49151	Amino acid sequenc
528	5	10.2	332	21	G37924	Arabidopsis thalia	601	5	10.2	412	18	W20789	H. pylori cytoplas
529	5	10.2	332	21	Y74739	Neisseria meningit	602	5	10.2	414	21	G30649	Arabidopsis thalia
530	5	10.2	336	20	Y19968	B. burgdorferi ant	603	5	10.2	416	21	G43150	Arabidopsis thalia
531	5	10.2	337	21	G41778	Arabidopsis thalia	604	5	10.2	418	20	Y37459	Protein involved i
532	5	10.2	337	21	G52535	Arabidopsis thalia	605	5	10.2	418	21	G59030	Arabidopsis thalia
533	5	10.2	343	12	R13276	Tobacco extracellu	606	5	10.2	419	18	W20872	H. pylori secreted
534	5	10.2	343	18	W31298	Nicotiana sp. extr	607	5	10.2	419	20	Y49243	N-terminal region
535	5	10.2	343	21	B07514	Amino acid sequenc	608	5	10.2	419	20	Y32182	N-terminal choline
536	5	10.2	343	21	G52534	Arabidopsis thalia	609	5	10.2	419	20	Y49149	Amino acid sequenc
537	5	10.2	343	21	Y44577	Xylitol dehydrogen	610	5	10.2	419	21	G18199	Arabidopsis thalia
538	5	10.2	344	21	W06611	Human porphobilino	611	5	10.2	419	21	G27322	Arabidopsis thalia
539	5	10.2	344	20	G27323	Arabidopsis thalia	612	5	10.2	419	21	G50028	Human heregulin-be
540	5	10.2	348	20	Y25806	Human secreted pro	613	5	10.2	420	13	R29375	Herugelin-beta-2-l
541	5	10.2	350	21	G07251	Arabidopsis thalia	614	5	10.2	420	20	Y06638	Human Heregulin HR
542	5	10.2	350	21	G43383	Arabidopsis thalia	615	5	10.2	420	21	Y71175	Parasporium rhizob
543	5	10.2	354	21	G13829	Arabidopsis thalia	616	5	10.2	422	6	P50775	Rat NR5F. Rattus
544	5	10.2	354	21	G29125	Arabidopsis thalia	617	5	10.2	422	14	R43651	Human NR5F. Homo
545	5	10.2	361	20	Y30874	Human secreted pro	618	5	10.2	422	14	R51269	GGR-II encoded by
546	5	10.2	364	21	G51816	Arabidopsis thalia	619	5	10.2	422	15	R56554	GGR-II encoded by
547	5	10.2	364	21	G52519	Arabidopsis thalia	620	5	10.2	422	15	R46923	Rat NDF. Rattus r
548	5	10.2	366	21	G08189	Arabidopsis thalia	621	5	10.2	422	16	R68569	Rat NDF. Rattus r
549	5	10.2	366	21	G43152	Arabidopsis thalia	622	5	10.2	422	16	R68568	Human glial cell g
550	5	10.2	368	21	G07250	Arabidopsis thalia	623	5	10.2	422	15	R67258	Human neuregulin G
551	5	10.2	368	21	G43382	Arabidopsis thalia	624	5	10.2	422	17	W09371	Human GGF2. Homo
552	5	10.2	369	21	G20759	Arabidopsis thalia	625	5	10.2	422	17	W09372	Human GGF2. Homo
553	5	10.2	372	22	B28788	Protein encoded by	626	5	10.2	422	17	R96081	Glial growth facto
554	5	10.2	373	21	Y99446	Human PRO1781 (UNQ	627	5	10.2	422	17	R87466	Glial growth facto
555	5	10.2	374	21	G06826	Arabidopsis thalia	628	5	10.2	422	17	R87467	Glial growth facto
556	5	10.2	374	21	G49382	Arabidopsis thalia	629	5	10.2	422	17	R86628	Mature hGF2. Hom
557	5	10.2	376	20	Y37222	Protein which is s	630	5	10.2	425	20	Y49248	N-terminal region
558	5	10.2	377	21	G45774	Arabidopsis thalia	631	5	10.2	425	20	Y32187	N-terminal choline
559	5	10.2	378	17	R99796	Biotin synthetis e	632	5	10.2	425	21	G41889	Arabidopsis thalia
560	5	10.2	378	20	W73908	A. thaliana biotin	633	5	10.2	426	21	G41777	Arabidopsis thalia
561	5	10.2	378	21	G45773	Arabidopsis thalia	634	5	10.2	426	22	B36588	Human FLEXHM-10 pr
562	5	10.2	379	21	Y15155	Human prostate ser	635	5	10.2	430	21	G21312	Arabidopsis thalia
563	5	10.2	383	21	G20551	Arabidopsis thalia	636	5	10.2	430	21	G51814	Arabidopsis thalia
564	5	10.2	383	21	G50026	Arabidopsis thalia	637	5	10.2	430	21	G54147	Arabidopsis thalia
565	5	10.2	384	21	G08346	Arabidopsis thalia	638	5	10.2	433	20	Y49245	N-terminal region
566	5	10.2	384	21	G32581	Arabidopsis thalia	639	5	10.2	433	20	Y32184	N-terminal choline
567	5	10.2	384	21	G51391	Arabidopsis thalia	640	5	10.2	433	21	G48155	Arabidopsis thalia
568	5	10.2	385	21	G08345	Arabidopsis thalia	641	5	10.2	434	20	Y13567	Human Robo 2 polyp
569	5	10.2	385	21	G32580	Arabidopsis thalia	642	5	10.2	434	20	Y08405	Human partial ROBO
570	5	10.2	385	21	G51390	Arabidopsis thalia	643	5	10.2	436	15	R56658	Aminopeptidase pep
571	5	10.2	391	21	G18198	Chlamydia pneumoni	644	5	10.2	436	19	Y11029	H. pylori ORF 01cp
572	5	10.2	391	21	G18198	Arabidopsis thalia	645	5	10.2	451	14	R31184	GABA-A receptor al
573	5	10.2	391	21	G45868	Arabidopsis thalia	646	5	10.2	451	15	R59862	Human GABA recepto
574	5	10.2	392	21	G18197	Arabidopsis thalia	647	5	10.2	451	18	W16328	Human host cell pr
575	5	10.2	392	21	G45867	Arabidopsis thalia	648	5	10.2	453	21	G21311	Arabidopsis thalia
576	5	10.2	393	21	G35663	Arabidopsis thalia	649	5	10.2	453	21	G54146	Arabidopsis thalia
577	5	10.2	393	21	G51815	Arabidopsis thalia	650	5	10.2	455	15	R57771	Mouse nucleobindin
578	5	10.2	393	21	G52518	Arabidopsis thalia	651	5	10.2	456	19	W77355	Altered telomere r
579	5	10.2	394	21	G05314	Arabidopsis thalia	652	5	10.2	456	19	W48628	Rat liver ribonucle
580	5	10.2	394	21	G39979	Arabidopsis thalia	653	5	10.2	456	21	G41776	Arabidopsis thalia
581	5	10.2	395	21	G13828	Arabidopsis thalia	654	5	10.2	457	21	G10061	Arabidopsis thalia
582	5	10.2	396	21	B26416	Drosophila melanog	655	5	10.2	461	16	R68572	Rat NDF encoded by
583	5	10.2	396	21	B20920	Drosophila odorant	656	5	10.2	461	16	R68571	Rat NDF encoded by
584	5	10.2	398	21	G29696	Arabidopsis thalia	657	5	10.2	461	21	G25647	Arabidopsis thalia
585	5	10.2	400	18	W20375	H. pylori secreted	658	5	10.2	462	16	R68562	Human NDF-alpha2b
586	5	10.2	400	21	G20550	Arabidopsis thalia	659	5	10.2	462	16	R68561	Human prNDF-alpha
587	5	10.2	400	21	G50025	Arabidopsis thalia	660	5	10.2	463	21	B16688	Bacteriophage bp-1
588	5	10.2	402	21	G08188	Arabidopsis thalia	661	5	10.2	463	21	G30392	Arabidopsis thalia
589	5	10.2	402	21	G39978	Arabidopsis thalia	662	5	10.2	463	21	B57042	Human prostate can
590	5	10.2	402	21	G43151	Arabidopsis thalia	663	5	10.2	468	21	G10060	Arabidopsis thalia
591	5	10.2	403	21	G05313	Arabidopsis thalia	664	5	10.2	473	21	B42243	Human ORFX ORF2007
592	5	10.2	403	21	G18200	Arabidopsis thalia	665	5	10.2	474	14	R31582	Sequence encoded b
593	5	10.2	403	21	G50029	Arabidopsis thalia	666	5	10.2	474	18	W39084	Human ShcC mutant
594	5	10.2	404	21	G13827	Arabidopsis thalia	667	5	10.2	474	18	W39085	Human ShcC mutant
595	5	10.2	404	21	G18196	Arabidopsis thalia	668	5	10.2	474	18	W39086	Human ShcC mutant

669	5	10.2	474	18	W39088	Human ShcC mutant	742	5	10.2	578	19	W40042	Biologically equiv
670	5	10.2	474	18	W39089	Human ShcC mutant	743	5	10.2	578	19	W40043	Biologically equiv
671	5	10.2	474	18	W39090	Human ShcC mutant	744	5	10.2	578	19	W40044	Biologically equiv
672	5	10.2	474	18	W39091	Human ShcC mutant	745	5	10.2	578	19	W40045	Biologically equiv
673	5	10.2	474	18	W39092	Human ShcC mutant	746	5	10.2	581	20	Y42774	Rat neuronal immed
674	5	10.2	474	18	W39093	Human ShcC mutant	747	5	10.2	584	20	Y15222	Human receptor pro
675	5	10.2	474	18	W39094	Human ShcC mutant	748	5	10.2	586	11	R07998	Asparagine synthet
676	5	10.2	474	18	W39096	Human ShcC mutant	749	5	10.2	586	21	B27304	A. thaliana N1M1 h
677	5	10.2	474	18	W23246	Human ShcC protein	750	5	10.2	587	21	G41887	Arabidopsis thalia
678	5	10.2	474	18	W39087	Human ShcC mutant	751	5	10.2	587	21	G52977	Arabidopsis thalia
679	5	10.2	474	18	W15253	Human brain-specific	752	5	10.2	588	21	G49517	Arabidopsis thalia
680	5	10.2	474	18	W15257	Rat brain-specific	753	5	10.2	591	18	W37399	Human sex comb on
681	5	10.2	476	18	W24089	Balanus amphitrite	754	5	10.2	591	18	W37395	Human sex comb on
682	5	10.2	479	21	G25646	Arabidopsis thalia	755	5	10.2	591	20	Y18289	Human Ssm protein
683	5	10.2	479	21	G41888	Arabidopsis thalia	756	5	10.2	593	19	W98782	H. pylori GPO 120
684	5	10.2	482	21	B18316	Plasmodium falcipa	757	5	10.2	594	18	W15260	Rat brain-specific
685	5	10.2	482	21	B18316	S. aureus D1A prote	758	5	10.2	594	18	W15256	Human brain-specif
686	5	10.2	487	16	R79906	Human histamine H1	759	5	10.2	595	16	R81314	Yeast T1H1. Sacch
687	5	10.2	487	16	R79905	Human histamine H1	760	5	10.2	595	19	W54167	S. cerevisiae T1H1
688	5	10.2	488	21	R83288	Borrelia antigenic	761	5	10.2	595	20	W87487	S. cerevisiae T1H1
689	5	10.2	491	14	R36979	Histamine H1 recep	762	5	10.2	603	19	W40040	A. Haemophilus infl
690	5	10.2	491	15	R48059	Sequence of protea	763	5	10.2	615	16	R74630	Tomato TGERP1 ethy
691	5	10.2	496	21	R25531	Eucalyptus grandis	764	5	10.2	615	19	W73126	Tomato ethylene re
692	5	10.2	498	15	R55800	Interleukin 14. H	765	5	10.2	619	16	R77545	MEKK2 protein. Mu
693	5	10.2	499	20	W30648	A. thaliana xylan	766	5	10.2	619	19	W56158	A Mitogen-activate
694	5	10.2	500	19	W77356	Human telomere rep	767	5	10.2	619	20	Y43319	Mitogen ERK kinase
695	5	10.2	500	20	Y02185	A human telomere r	768	5	10.2	619	20	Y42108	Murine MEKK2 prote
696	5	10.2	501	20	Y17293	Mouse cell death p	769	5	10.2	619	20	W73532	MEKK2 protein. Ma
697	5	10.2	501	20	Y01097	PREA11 protein.	770	5	10.2	619	21	B01217	Murine MEKK2. Mus
698	5	10.2	501	21	G53411	Arabidopsis thalia	771	5	10.2	620	18	W37397	Human sex comb on
699	5	10.2	501	21	Y54311	Amino acid sequenc	772	5	10.2	620	18	W37393	Human Ssm protein
700	5	10.2	502	20	Y17292	Human cell death p	773	5	10.2	620	20	Y18287	Human sex comb on
701	5	10.2	503	21	G35662	Arabidopsis thalia	774	5	10.2	620	21	G32089	Arabidopsis thalia
702	5	10.2	503	21	G52517	Arabidopsis thalia	775	5	10.2	622	21	G06559	Arabidopsis thalia
703	5	10.2	504	21	G38853	Arabidopsis thalia	776	5	10.2	625	20	Y06834	Herugelin-alpha.
704	5	10.2	509	21	Y91965	PWAV-1 heat shock	777	5	10.2	626	21	G06558	Arabidopsis thalia
705	5	10.2	513	21	G27321	Arabidopsis thalia	778	5	10.2	633	21	B25492	Eucalyptus grandis
706	5	10.2	519	21	Y44247	Human cell signall	779	5	10.2	636	16	R68576	Rat NDF encoded by
707	5	10.2	521	20	Y30794	Amino acid sequenc	780	5	10.2	636	16	R68573	Rat NDF encoded by
708	5	10.2	522	21	G38852	Arabidopsis thalia	781	5	10.2	637	13	R29573	Human heregulin-be
709	5	10.2	526	19	W48445	Cyclomaltodextrin	782	5	10.2	637	20	Y06836	Herugelin-beta-2.
710	5	10.2	527	19	W48418	Human gamma-heregu	783	5	10.2	637	21	Y11173	Human Heregulin HR
711	5	10.2	532	21	G35661	Arabidopsis thalia	784	5	10.2	639	16	R68578	Rat NDF encoded by
712	5	10.2	543	19	W72196	HSV-2 strain SB5 C	785	5	10.2	639	16	R68574	Rat NDF encoded by
713	5	10.2	549	15	R66030	Mammalian MEK kina	786	5	10.2	642	15	R51620	FelV gp70 and p15E
714	5	10.2	550	21	B41552	Human ORFX ORF1316	787	5	10.2	642	21	B42738	Human ORFX ORF2502
715	5	10.2	551	21	Y55836	Mouse SPOT01 poly	788	5	10.2	645	20	Y06635	Herugelin-beta-1.
716	5	10.2	552	20	W96299	vgaB streptogramin	789	5	10.2	645	21	B36793	Human heregulin-be
717	5	10.2	553	20	Y55721	Human forkhead tra	790	5	10.2	646	21	G30550	Arabidopsis thalia
718	5	10.2	553	20	Y41277	Human FREAC3 prote	791	5	10.2	646	21	G51610	Arabidopsis thalia
719	5	10.2	553	20	Y43260	Human FKHL7 protei	792	5	10.2	649	21	G32088	Arabidopsis thalia
720	5	10.2	555	21	G49519	Arabidopsis thalia	793	5	10.2	652	20	Y39225	M. tuberculosis fu
721	5	10.2	563	21	G49518	Arabidopsis thalia	794	5	10.2	652	20	Y39082	M. tuberculosis fus
722	5	10.2	565	21	B43718	Human cancer assoc	795	5	10.2	652	21	G51609	Arabidopsis thalia
723	5	10.2	571	21	B57095	Human prostate can	796	5	10.2	656	21	G51804	Arabidopsis thalia
724	5	10.2	571	21	B16603	Bacteriophage 192	797	5	10.2	659	21	B38516	Fragment of human
725	5	10.2	576	20	Y49541	Human PRO201 (Nsp1	798	5	10.2	659	21	G39867	Arabidopsis thalia
726	5	10.2	576	20	Y49545	Human Nsp1 mutant	799	5	10.2	662	16	R68577	Rat NDF encoded by
727	5	10.2	576	20	Y49546	Human Nsp1 mutant	800	5	10.2	664	18	W37400	Mouse sex comb on
728	5	10.2	576	20	Y49547	Human Nsp1 mutant	801	5	10.2	664	18	W37396	Mouse sex comb on
729	5	10.2	576	20	Y06477	Human tumour-assoc	802	5	10.2	664	20	Y18290	Mouse Ssm protein
730	5	10.2	576	21	Y93684	Amino acid sequenc	803	5	10.2	664	21	G32092	Arabidopsis thalia
731	5	10.2	576	21	Y51932	Human PRO201 prote	804	5	10.2	664	21	G52976	Arabidopsis thalia
732	5	10.2	577	18	Y51939	Human sex comb on	805	5	10.2	666	21	G30549	Arabidopsis thalia
733	5	10.2	577	18	W37398	Human sex comb on	806	5	10.2	668	21	G30591	Arabidopsis thalia
734	5	10.2	577	18	W37394	Human Ssm protein	807	5	10.2	669	13	R29570	Arabidopsis thalia
735	5	10.2	578	19	W40046	Biologically equiv	808	5	10.2	669	21	Y11171	Human heregulin-al
736	5	10.2	578	19	W40047	Biologically equiv	809	5	10.2	673	20	W30641	Human Heregulin HR
737	5	10.2	578	19	W40048	Biologically equiv	810	5	10.2	673	21	G52975	Arabidopsis thalia
738	5	10.2	578	19	W40049	Biologically equiv	811	5	10.2	674	21	G16608	Arabidopsis thalia
739	5	10.2	578	19	W40050	Biologically equiv	812	5	10.2	674	21	G49526	Arabidopsis thalia
740	5	10.2	578	19	W40051	Biologically equiv	813	5	10.2	675	13	R29571	Human heregulin-be
741	5	10.2	578	19	W40041	Biologically equiv	814	5	10.2	675	19	W74487	Amino acid sequenc

815	5	10.2	675	19	W74488	Amino acid sequenc	888	5	10.2	683	17	W17645	Thermoanaerobacter
816	5	10.2	675	19	W74486	Amino acid sequenc	889	5	10.2	683	17	W17646	CGTase variant 146
817	5	10.2	675	19	W74485	Degenerate amino a	890	5	10.2	683	17	W17647	CGTase variant 145
818	5	10.2	675	19	W74504	Amino acid sequenc	891	5	10.2	683	17	W17648	CGTase variant 145
819	5	10.2	675	19	W74503	Amino acid sequenc	892	5	10.2	683	17	W17651	Thermoanaerobacter
820	5	10.2	675	19	W74502	Amino acid sequenc	893	5	10.2	683	17	W17622	Thermoanaerobacter
821	5	10.2	675	19	W74501	Amino acid sequenc	894	5	10.2	683	17	W17623	Thermoanaerobacter
822	5	10.2	675	19	W74500	Amino acid sequenc	895	5	10.2	683	17	W17624	Thermoanaerobacter
823	5	10.2	675	19	W74499	Amino acid sequenc	896	5	10.2	683	17	W17625	Thermoanaerobacter
824	5	10.2	675	19	W74498	Amino acid sequenc	897	5	10.2	683	17	W17626	Thermoanaerobacter
825	5	10.2	675	19	W74497	Amino acid sequenc	898	5	10.2	683	17	W17627	Thermoanaerobacter
826	5	10.2	675	19	W74496	Amino acid sequenc	899	5	10.2	683	17	W17628	Thermoanaerobacter
827	5	10.2	675	19	W74495	Amino acid sequenc	900	5	10.2	683	17	W17629	Thermoanaerobacter
828	5	10.2	675	19	W74494	Amino acid sequenc	901	5	10.2	683	17	W17630	Thermoanaerobacter
829	5	10.2	675	19	W74493	Amino acid sequenc	902	5	10.2	683	17	W17631	Thermoanaerobacter
830	5	10.2	675	19	W74492	Amino acid sequenc	903	5	10.2	683	17	W17632	Thermoanaerobacter
831	5	10.2	675	19	W74491	Amino acid sequenc	904	5	10.2	683	17	W17633	Thermoanaerobacter
832	5	10.2	675	19	W74490	Amino acid sequenc	905	5	10.2	683	17	W17610	Thermoanaerobacter
833	5	10.2	675	19	W74489	Amino acid sequenc	906	5	10.2	683	17	W17613	Thermoanaerobacter
834	5	10.2	675	19	W74509	Amino acid sequenc	907	5	10.2	683	17	W17614	Thermoanaerobacter
835	5	10.2	675	19	W74508	Amino acid sequenc	908	5	10.2	683	17	W17616	Thermoanaerobacter
836	5	10.2	675	19	W74507	Amino acid sequenc	909	5	10.2	683	17	W17617	Thermoanaerobacter
837	5	10.2	675	19	W74506	Amino acid sequenc	910	5	10.2	683	17	W17634	Thermoanaerobacter
838	5	10.2	675	19	W74505	Amino acid sequenc	911	5	10.2	683	17	W17635	Thermoanaerobacter
839	5	10.2	675	21	W71172	Human Heregulin HR	912	5	10.2	683	17	W17636	Thermoanaerobacter
840	5	10.2	675	21	W71178	Human Heregulin HR	913	5	10.2	683	17	W17618	Thermoanaerobacter
841	5	10.2	675	21	W71179	Human Heregulin HR	914	5	10.2	683	17	W17619	Thermoanaerobacter
842	5	10.2	675	21	W71180	Human Heregulin HR	915	5	10.2	683	17	W17620	Thermoanaerobacter
843	5	10.2	675	21	W71181	Human Heregulin HR	916	5	10.2	684	17	W17621	Thermoanaerobacter
844	5	10.2	675	21	W71182	Human Heregulin HR	917	5	10.2	684	17	W17580	Thermoanaerobacter
845	5	10.2	675	21	W71183	Human Heregulin HR	918	5	10.2	684	17	W17581	Thermoanaerobacter
846	5	10.2	675	21	W71184	Human Heregulin HR	919	5	10.2	684	17	W17583	Thermoanaerobacter
847	5	10.2	675	21	W71185	Human Heregulin HR	920	5	10.2	684	17	W17584	Thermoanaerobacter
848	5	10.2	675	21	W71186	Human Heregulin HR	921	5	10.2	684	17	W17585	Thermoanaerobacter
849	5	10.2	675	21	W71187	Human Heregulin HR	922	5	10.2	684	17	W17587	Thermoanaerobacter
850	5	10.2	675	21	W71188	Human Heregulin HR	923	5	10.2	684	17	W17588	Thermoanaerobacter
851	5	10.2	675	21	W71189	Human Heregulin HR	924	5	10.2	684	17	W17589	Thermoanaerobacter
852	5	10.2	675	21	W71190	Human Heregulin HR	925	5	10.2	684	17	W17591	Thermoanaerobacter
853	5	10.2	675	21	W71191	Human Heregulin HR	926	5	10.2	685	17	W17582	Thermoanaerobacter
854	5	10.2	675	21	W71192	Human Heregulin HR	927	5	10.2	685	17	W17586	Thermoanaerobacter
855	5	10.2	675	21	W71193	Human Heregulin HR	928	5	10.2	685	17	W17590	Thermoanaerobacter
856	5	10.2	675	21	W71194	Human Heregulin HR	929	5	10.2	685	21	G51803	Arabidopsis thalia
857	5	10.2	675	21	W71195	Human Heregulin HR	930	5	10.2	686	21	G32087	Arabidopsis thalia
858	5	10.2	675	21	W71196	Human Heregulin HR	931	5	10.2	689	19	W98483	H. pylori GHP0 992
859	5	10.2	675	21	W71197	Human Heregulin HR	932	5	10.2	690	21	G30548	Arabidopsis thalia
860	5	10.2	675	21	W71198	Human Heregulin HR	933	5	10.2	692	21	G30390	Arabidopsis thalia
861	5	10.2	675	21	W71199	Human Heregulin HR	934	5	10.2	693	21	G32091	Arabidopsis thalia
862	5	10.2	675	21	W71200	Human Heregulin HR	935	5	10.2	699	21	G16607	Arabidopsis thalia
863	5	10.2	675	21	W71201	Human Heregulin HR	936	5	10.2	699	21	G49525	Arabidopsis thalia
864	5	10.2	675	21	W71202	Human Heregulin HR	937	5	10.2	702	14	R40810	ADA3. Synthetic.
865	5	10.2	675	21	W71203	Human Heregulin HR	938	5	10.2	704	12	R14204	Cyclodextrin gluca
866	5	10.2	677	19	W55984	Swinepox virus str	939	5	10.2	704	12	R15313	Cyclodextrin gluca
867	5	10.2	679	17	W17650	CGTase variant 87-	940	5	10.2	704	12	R15314	Cyclodextrin gluca
868	5	10.2	679	17	W17652	CGTase variant 87-	941	5	10.2	704	12	R11217	Cyclodextrin gluca
869	5	10.2	681	17	W17607	Thermoanaerobacter	942	5	10.2	704	14	R41248	B.ohbensis mutant
870	5	10.2	681	17	W17615	Thermoanaerobacter	943	5	10.2	704	14	R41249	B.ohbensis Alai88
871	5	10.2	682	17	W17638	CGTase variant 87-	944	5	10.2	704	14	R41250	B.ohbensis Ser188
872	5	10.2	682	17	W17639	CGTase variant 87-	945	5	10.2	704	14	R41251	B.ohbensis Trp188
873	5	10.2	682	17	W17649	CGTase variant 87-	946	5	10.2	722	20	W86308	Kidney injury asso
874	5	10.2	682	17	W17606	Thermoanaerobacter	947	5	10.2	722	21	G51802	Arabidopsis thalia
875	5	10.2	682	17	W17608	Thermoanaerobacter	948	5	10.2	725	21	G38851	Arabidopsis thalia
876	5	10.2	682	17	W17609	CGTase variant F19	949	5	10.2	728	21	G49524	Arabidopsis thalia
877	5	10.2	682	17	W17611	CGTase variant 87-	950	5	10.2	729	21	G16606	Arabidopsis thalia
878	5	10.2	682	17	W17612	CGTase variant 87-	951	5	10.2	730	21	G32090	Arabidopsis thalia
879	5	10.2	682	17	W17637	Thermoanaerobacter	952	5	10.2	734	21	G38557	Arabidopsis thalia
880	5	10.2	682	21	G25645	Arabidopsis thalia	953	5	10.2	740	20	Y25005	Meion MEETRI prote
881	5	10.2	682	21	G51608	Arabidopsis thalia	954	5	10.2	741	21	G38556	Arabidopsis thalia
882	5	10.2	683	17	W06772	Wild type cyclomal	955	5	10.2	746	20	Y28882	Human Ext-1 protei
883	5	10.2	683	17	W17640	Thermoanaerobacter	956	5	10.2	763	20	Y04741	PDZ domain-contain
884	5	10.2	683	17	W17641	Thermoanaerobacter	957	5	10.2	767	19	Y11030	H. pylori ORF Olcp
885	5	10.2	683	17	W17642	Thermoanaerobacter	958	5	10.2	767	20	Y17184	H. pylori outer me
886	5	10.2	683	17	W17643	Thermoanaerobacter	959	5	10.2	768	19	W44817	Human gamma-heragu
887	5	10.2	683	17	W17644	Thermoanaerobacter	960	5	10.2	768	20	Y06639	Gamma-heragulin.

961 Human Heregulin va 768 21 W71176
 962 Yeast mitochondria 777 18 W16304
 963 Grand fir monoterp 782 20 W85703
 964 Grand fir E-alpha- 782 21 Y90853
 965 Human OREF ORF1773 792 21 B42009
 966 HL60 cell line pro 793 19 W73307
 967 Soybean cellulose 793 21 Y58839
 968 Human integrin bet 798 22 B36937
 969 M. tuberculosis fu 802 19 W81746
 970 Mycobacterium anti 802 19 W64379
 971 Mycobacterium tube 802 20 Y32063
 972 M. tuberculosis fu 802 20 Y32224
 973 M. tuberculosis fu 802 20 Y39176
 974 M. tuberculosis fu 802 20 Y39081
 975 M. tuberculosis fu 802 20 Y39033
 976 Plasmodium falcipa 807 21 B18311
 977 Grand fir E-alpha- 817 20 Y06562
 978 Grand fir E-alpha- 817 20 Y06566
 979 E-alpha-bisabolene 817 20 Y06567
 980 E-alpha-bisabolene 817 20 Y06568
 981 Porphyromonas ging 834 20 Y34542
 982 Porphyromonas ging 853 21 B00052
 983 Human sperm protei 856 21 B01383
 984 Neuron-associated 856 21 B01383
 985 Arabidopsis thalia 856 21 B01383
 986 Arabidopsis thalia 893 21 G38539
 987 Moraxella catarrha 905 20 W89421
 988 Porphyromonas ging 907 20 Y34408
 989 Pol region gene pr 917 16 R64974
 990 Human cytomegalovi 946 18 W27085
 991 Human cytomegalovi 946 18 W27084
 992 Mouse SMAD interac 950 20 W83319
 993 Yeast MSH1 protein 959 16 R76066
 994 Integrin beta-1 ch 963 19 W70540
 995 Yeast MSH1 protein 971 16 R76070
 996 Mature protein con 1005 20 Y04731
 997 Arabidopsis thalia 1017 21 G38537
 998 Arabidopsis thalia 1024 21 G47319
 999 Arabidopsis thalia 1025 21 G38555
 1000 Protein L. Peptoc 1027 14 R42203
 1001 Protein L. Peptoc 1027 14 R43699

ALIGNMENTS

RESULT 1
 W39217
 ID W39217 standard; peptide: 49 AA.
 XX W39217;
 AC W39217;
 DT 27-AUG-1998 (first entry)
 XX 27-AUG-1998 (first entry)
 DE Human RSV A subtype G protein fragment (aa. 149-157) strain A2.
 XX
 KW G protein; treatment; prevention; diagnosis; infection; immunity;
 KW antibody; Pneumovirus; identification; vaccine; cell receptor.
 XX
 OS Human respiratory syncytial virus.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 25..38
 FT Disulfide-bond 28..34
 XX
 PN W09746581-A1.
 XX
 PD 11-DEC-1997.
 XX
 PF 04-JUN-1997; 97WO-AU00351.
 XX
 PR 05-JUN-1996; 96AU-0000265.
 XX
 PA (BIOM-) BIOMOLECULAR RES INST LTD.

XX Gorman JJ;
 PI WPI; 1998-042117/04.
 XX
 DR Peptide(s) derived from specific region of respiratory syncytial
 XX virus G protein - used to treat, prevent, diagnose and immunise
 PT against Pneumovirus infection
 PT
 XX Claim 5; Fig 2; 75pp; English.
 PS
 CC W39217-W39234 are fragments of the human respiratory syncytial virus
 CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments
 CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
 CC infection and to immunise against such infections. Antibodies raised
 CC from these fragments may also be used diagnostically. The fragments may
 CC also be used to identify compounds able to inhibit binding of RSV to host
 CC cells and for characterisation of cell receptors for Pneumoviruses. When
 CC the fragments are used in combination with existing vaccines, they may
 CC allow a reduction in dose, and thus side effects, of the vaccine.
 XX
 SQ Sequence 49 AA;
 Query Match 100.0%; Score 49; DB 19; Length 49;
 Best Local Similarity 100.0%; Pred. No. 1.4e-43;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KORQNKPSKPNNDHFEVFNVPSCISNNPTCWAICKRIPNKKPGKK 49
 DB 1 KQRQKPSKPNNDHFEVFNVPSCISNNPTCWAICKRIPNKKPGKK 49
 RESULT 2
 W39244
 ID W39244 standard; peptide: 49 AA.
 XX W39244;
 AC W39244;
 XX 27-AUG-1998 (first entry)
 DT 27-AUG-1998 (first entry)
 XX
 DE Human RSV G protein fragment (aa. 149-157) derivative #1.
 XX
 KW G protein; treatment; prevention; diagnosis; infection; immunity;
 KW antibody; Pneumovirus; identification; vaccine; cell receptor.
 XX
 OS Human respiratory syncytial virus.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT Modified-site /note= "N-terminal acetylated"
 FT Disulfide-bond 25..38
 FT Disulfide-bond 28..34
 FT Modified-site 49
 FT Modified-site /note= "C-terminal amide"
 XX
 PN W09746581-A1.
 XX
 PD 11-DEC-1997.
 XX
 PF 04-JUN-1997; 97WO-AU00351.
 XX
 PR 05-JUN-1996; 96AU-0000265.
 XX
 PA (BIOM-) BIOMOLECULAR RES INST LTD.
 XX
 PI Gorman JJ;
 XX
 DR WPI; 1998-042117/04.
 XX
 PT Peptide(s) derived from specific region of respiratory syncytial
 PT virus G protein - used to treat, prevent, diagnose and immunise
 PT against Pneumovirus infection
 PT

XX Example 4; Fig 12; 75pp; English.

XX W39244-W39252 are derivatives of the human respiratory syncytial virus

CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments

CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,

CC infection and to immunise against such infections. Antibodies raised

CC from these fragments may also be used diagnostically. The fragments may

CC also be used to identify compounds able to inhibit binding of RSV to host

CC cells and for characterisation of cell receptors for Pneumoviruses. When

CC the fragments are used in combination with existing vaccines, they may

CC allow a reduction in dose, and thus side effects, of the vaccine.

XX Sequence 49 AA;

SQ

Query Match 100.0%; Score 49; DB 19; Length 49;

Best Local Similarity 100.0%; Pred. No. 1.4e-43; Indels 0; Gaps 0;

Matches 49; Conservative 0; Mismatches 0;

QY 1 KORQKPPSKPNDFHFVFNPCISCSNNPTCWAICKRIPNKKPGKK 49

|||||

Db 1 kqrqkppskpnndhfefvfnpciscsnnptcwaickripnkkpgkk 49

RESULT 3

W39248

ID W39248 standard; peptide; 49 AA.

XX

AC W39248;

XX

DT 27-AUG-1998 (first entry)

XX

DE Human RSV G protein fragment (aa. 149-157) derivative #5.

XX

KW G protein; treatment; prevention; diagnosis; infection; immunity;

KW antibody; Pneumovirus; identification; vaccine; cell receptor.

XX

OS Human respiratory syncytial virus.

XX

FH Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal fitc group"

FT Disulfide-bond 25..38

FT Disulfide-bond 28..34

FT Modified-site 49

FT /note= "C-terminal amide"

XX

PN W09746581-AL.

XX

PD 11-DEC-1997.

XX

PF 04-JUN-1997; 97WO-AU00351.

XX

PR 05-JUN-1996; 96AU-0000265.

XX

PA (BIOM-) BIOMOLECULAR RES INST LTD.

XX

PI Gorman JJ;

XX

DR WPI; 1998-042117/04.

XX

PT Peptide(s) derived from specific region of respiratory syncytial

PT virus G protein - used to treat, prevent, diagnose and immunise

PT against Pneumovirus infection

XX

PS Example 4; Fig 12; 75pp; English.

XX

W39244-W39252 are derivatives of the human respiratory syncytial virus

CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments

CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,

CC infection and to immunise against such infections. Antibodies raised

CC from these fragments may also be used diagnostically. The fragments may

CC also be used to identify compounds able to inhibit binding of RSV to host

CC cells and for characterisation of cell receptors for Pneumoviruses. When

CC the fragments are used in combination with existing vaccines, they may

CC allow a reduction in dose, and thus side effects, of the vaccine.

XX Sequence 49 AA;

SQ

Query Match 100.0%; Score 49; DB 19; Length 49;

Best Local Similarity 100.0%; Pred. No. 1.4e-43; Indels 0; Gaps 0;

Matches 49; Conservative 0; Mismatches 0;

QY 1 KORQKPPSKPNDFHFVFNPCISCSNNPTCWAICKRIPNKKPGKK 49

|||||

Db 1 kqrqkppskpnndhfefvfnpciscsnnptcwaickripnkkpgkk 49

RESULT 4

W39250

ID W39250 standard; peptide; 49 AA.

XX

AC W39250;

XX

DT 27-AUG-1998 (first entry)

XX

DE Human RSV G protein fragment (aa. 149-157) derivative #7.

XX

KW G protein; treatment; prevention; diagnosis; infection; immunity;

KW antibody; Pneumovirus; identification; vaccine; cell receptor.

XX

OS Human respiratory syncytial virus.

XX

FH Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal bb group"

FT Disulfide-bond 25..38

FT Disulfide-bond 28..34

FT Modified-site 49

FT /note= "C-terminal amide"

XX

PN W09746581-AL.

XX

PD 11-DEC-1997.

XX

PF 04-JUN-1997; 97WO-AU00351.

XX

PR 05-JUN-1996; 96AU-0000265.

XX

PA (BIOM-) BIOMOLECULAR RES INST LTD.

XX

PI Gorman JJ;

XX

DR WPI; 1998-042117/04.

XX

PT Peptide(s) derived from specific region of respiratory syncytial

PT virus G protein - used to treat, prevent, diagnose and immunise

PT against Pneumovirus infection

XX

PS Example 4; Fig 12; 75pp; English.

XX

W39244-W39252 are derivatives of the human respiratory syncytial virus

CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments

CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,

CC infection and to immunise against such infections. Antibodies raised

CC from these fragments may also be used diagnostically. The fragments may

CC also be used to identify compounds able to inhibit binding of RSV to host

CC cells and for characterisation of cell receptors for Pneumoviruses. When

CC the fragments are used in combination with existing vaccines, they may

CC allow a reduction in dose, and thus side effects, of the vaccine.

XX Sequence 49 AA;

SQ

Query Match 100.0%; Score 49; DB 19; Length 49;
 Best Local Similarity 100.0%; Pred. No. 1.4e-43;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORONKPPSKPNNDFEVEFVPCISNNPTCWAICKRIPNKPGKK 49
 |||||
 Db 1 kqrqkpskpndfhefvnfvpcisnnpctwaickripnkpgkk 49

RESULT 5
 W39251
 ID W39251 standard; peptide; 49 AA.
 AC W39251;
 XX
 DT 27-AUG-1998 (first entry)
 XX
 DE Human RSV G protein fragment (aa. 149-157) derivative #8.
 KW G protein; treatment; prevention; diagnosis; infection; immunity;
 KW antibody; Pneumovirus; identification; vaccine; cell receptor.
 XX
 OS Human respiratory syncytial virus.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-terminal biot group"
 FT Disulfide-bond 25..38
 FT Disulfide-bond 28..34
 FT Modified-site 49
 FT /note= "C-terminal amide"
 FT
 XX WO9746581-A1.
 PN 11-DEC-1997.
 XX
 PD 04-JUN-1997; 97WO-AU00351.
 PF
 XX 05-JUN-1996; 96AU-0000265.
 PR
 XX (BIOM-) BIOMOLECULAR RES INST LTD.
 PA
 XX
 PI
 XX
 DR WPI; 1998-042117/04.
 XX
 PT Peptide(s) derived from specific region of respiratory syncytial
 PT virus G protein - used to treat, prevent, diagnose and immunise
 PT against Pneumovirus infection
 XX
 PS Example 4; Fig 12; 75pp; English.
 XX
 CC W39244-W39252 are derivatives of the human respiratory syncytial virus
 CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments
 CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
 CC infection and to immunise against such infections. Antibodies raised
 CC from these fragments may also be used diagnostically. The fragments may
 CC also be used to identify compounds able to inhibit binding of RSV to host
 CC cells and for characterisation of cell receptors for Pneumoviruses. When
 CC the fragments are used in combination with existing vaccines, they may
 CC allow a reduction in dose, and thus side effects, of the vaccine.
 XX
 SQ Sequence 49 AA;

Query Match 100.0%; Score 49; DB 19; Length 49;
 Best Local Similarity 100.0%; Pred. No. 1.4e-43;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORONKPPSKPNNDFEVEFVPCISNNPTCWAICKRIPNKPGKK 49
 |||||
 Db 1 kqrqkpskpndfhefvnfvpcisnnpctwaickripnkpgkk 49

RESULT 6
 P70845
 ID P70845 standard; protein; 298 AA.
 XX
 AC P70845;
 XX
 DT 05-APR-1991 (first entry)
 XX
 DE Sequence of human respiratory syncytial virus (HRSV) A2 strain
 DE G protein.
 KW Vaccine.
 XX
 OS Human respiratory syncytial virus (HRSV).
 XX
 PN W08704185-A
 PD 16-JUL-1987.
 PF 23-DEC-1986; 86WO-US02756.
 XX
 PR 14-JAN-1986; 86US-0818740.
 XX
 PA (UXNC-) UNIV OF N CAROLINA.
 PA (WERTZ) WERTZ G.W.
 XX (WERTZ) WERTZ G.W.
 DR WPI; 1987-206300/29.
 DR N-PSDB; N70784.
 XX
 PT Vaccines for human respiratory virus - comprising proteins or
 PT fragment encoded by a DNA sequence coding for human respiratory
 PT syncytial virus proteins.
 XX
 PS Disclosure; Chart 13; 57pp; English.
 XX
 CC A novel plasmid which comprises a DNA sequence encoding this
 CC protein, and the protein itself, are claimed, for use as HRSV
 CC vaccines. The vaccine can be administered to pregnant women or to
 CC women of child bearing age to stimulate maternal antibodies.
 CC Infants can also be vaccinated at 2-3 months of age.
 XX
 SQ Sequence 298 AA.

Query Match 100.0%; Score 49; DB 8; Length 298;
 Best Local Similarity 100.0%; Pred. No. 5.7e-43;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORONKPPSKPNNDFEVEFVPCISNNPTCWAICKRIPNKPGKK 49
 |||||
 Db 149 kqrqkpskpndfhefvnfvpcisnnpctwaickripnkpgkk 197

RESULT 7
 R25302
 ID R25302 standard; Protein; 298 AA.
 XX
 AC R25302;
 XX
 DT 03-MAR-1993 (first entry)
 XX
 DE HSRV glycoprotein G (gpc).
 XX
 KW Vaccine; human respiratory syncytial virus; HRSV; F; G; 22K; 9.5K;
 KW major capsid protein; N.
 XX
 OS Human respiratory syncytial virus strain A2.
 XX
 PN G55149650-A
 PD 22-SEP-1992.

XX 14-JAN-1986; 86US-0818740.
 XX
 XX 14-JAN-1986; 86US-0818740.
 PR 13-JUL-1988; 88US-0218737.
 XX
 PA (UYN-) UNIV NORTH CAROLINA.
 XX
 XX Collins PL, Wertz GW;
 PI
 XX WPI; 1992-340247/41.
 DR N-PSDB; Q29623.
 XX

PT Vaccines for human respiratory virus - include structural genes
 PT coding for native structural viral proteins and immunogenic
 PT fragments
 XX

PS Disclosure; Page 18; 21pp; English.

XX The sequences of mRNA encoding HRSV structural proteins are given in
 CC Q29622-26. The proteins are F, G, 22K, 9.5K and major capsid
 CC protein N. The sequences and encoded proteins are useful for
 CC preparing vaccines against HRSV. The vaccines can be used to confer
 CC immunity against respiratory tract infections on human subjects.
 XX

XX Sequence 298 AA;

Query Match 100.0%; Score 49; DB 13; Length 298;
 Best Local Similarity 100.0%; Pred. No. 5.7e-43;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KORQKPPSKPNDHFHVFVPCISCSNNPTCWAICKRIPNKKPGKK 49
 Db 149 kqrqkppskpndhfefvfnfpcisnptcwaickripnkkpgkk 197

RESULT 8

W47605
 ID W47605 standard; Protein; 298 AA.

AC W47605;

XX 11-JUN-1998 (first entry)

XX HRSV glycoprotein G.

XX HRSV; glycoprotein F; gpF; glycoprotein G; gpG; vaccine.

XX Human respiratory syncytial virus.

XX US5716823-A.

XX 10-FEB-1998.

XX 12-MAY-1997; 97US-0854783.

XX 13-JUL-1988; 86US-0218737.

XX 14-JAN-1986; 86US-0818740.

XX 23-DEC-1986; 86WO-US02756.

XX 11-JUN-1992; 92US-0897171.

XX 12-MAY-1997; 97US-0854783.

XX (PHAA) PHARMACIA & UPJOHN CO.

XX Collins PL, Wertz GW;

XX WPI; 1998-144802/13.

XX N-PSDB; V18736.

XX Production of human respiratory syncytial virus glyco-protein F or G
 PT - by culturing eukaryotic host cells transfected with corresponding
 PT DNA.

XX Example 1; Columns 27-28; 17pp; English.
 XX
 XX The present sequence was used in the development of a novel method
 CC for the production of human respiratory syncytial virus (HRSV)
 CC glycoprotein F (gpF) or glycoprotein G (gpG). The method comprises
 CC culturing eukaryotic host cells transfected with an isolated DNA
 CC sequence encoding HRSV gpF or gpG. The gp can be used to prepare
 XX vaccines against HRSV.
 XX

SQ Sequence 298 AA;

Query Match 100.0%; Score 49; DB 19; Length 298;
 Best Local Similarity 100.0%; Pred. No. 5.7e-43;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KORQKPPSKPNDHFHVFVPCISCSNNPTCWAICKRIPNKKPGKK 49
 Db 149 kqrqkppskpndhfefvfnfpcisnptcwaickripnkkpgkk 197

RESULT 9

P90441
 ID P90441 standard; protein; 681 AA.

XX AC P90441;

XX 01-NOV-1989 (first entry)

XX Chimeric human respiratory syncytial virus glycoproteins F and G.

XX Chimeric polypeptide; human respiratory syncytial virus;

XX protein F; protein G; vaccine.

XX Human respiratory syncytial virus.

XX WO8905823-A.

XX 29-JUN-1989.

XX 31-OCT-1988; 88WO-US03784.

XX 23-DEC-1987; 87US-0137387.

XX (UPJO) UPJOHN CO.

XX Nathan M;

XX WPI; 1989-206593/28.

XX Chimeric human respiratory syncytial virus polypeptides(s)

XX - contg. immunogenic fragments from HRSV glycoproteins

XX F and G, for vaccine prodn.

XX Claim 3; page 47-48; 50pp; English.

XX Chimeric polypeptide contg. a signal sequence and one or more
 CC immunogenic fragments from both human respiratory syncytial virus
 CC glycoproteins F and G. Can be used in vaccines. Hosts are, eg
 CC E. coli, Chinese hamster ovary cells, murine C127 cells and
 CC S. frugiperda.
 XX

SQ Sequence 681 AA;

Query Match 100.0%; Score 49; DB 10; Length 681;
 Best Local Similarity 100.0%; Pred. No. 1.1e-42;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KORQKPPSKPNDHFHVFVPCISCSNNPTCWAICKRIPNKKPGKK 49
 Db 543 kqrqkppskpndhfefvfnfpcisnptcwaickripnkkpgkk 591

```

RESULT 10
W39219
ID W39219 standard; peptide; 49 AA.
XX
AC W39219;
XX
DT 27-AUG-1998 (first entry)
XX
DE Human RSV A subtype G protein fragment (aa. 149-157) strain A642.
XX
KW G protein; treatment; prevention; diagnosis; infection; immunity;
KW antibody; Pneumovirus; identification; vaccine; cell receptor.
XX
OS Human respiratory syncytial virus.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 25..38
FT Disulfide-bond 28..34
XX
PN WO9746581-A1.
XX
PD 11-DEC-1997.
XX
PF 04-JUN-1997; 97WO-AU00351.
XX
PR 05-JUN-1996; 96AU-0000265.
XX
PA (BIOM-) BIOMOLECULAR RES INST LTD.
XX
PI Gorman JJ;
XX
DR WPI; 1998-042117/04.
XX
PT Peptide(s) derived from specific region of respiratory syncytial
PT virus G protein - used to treat, prevent, diagnose and immunise
PT against Pneumovirus infection
XX
PS Claim 5; Fig 2; 75pp; English.
XX
CC W39217-W39234 are fragments of the human respiratory syncytial virus
CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments
CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
CC infection and to immunise against such infections. Antibodies raised
CC from these fragments may also be used diagnostically. The fragments may
CC also be used to identify compounds able to inhibit binding of RSV to host
CC cells and for characterisation of cell receptors for Pneumoviruses. When
CC the fragments are used in combination with existing vaccines, they may
CC allow a reduction in dose, and thus side effects, of the vaccine.
XX
SQ Sequence 49 AA;

Query Match 98.0%; Score 48; DB 19; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.5e-42;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQNKPPSKPNDFHFEVFNVPSCISCSNNPTCWAICKRIPNKKPGK 48
Db 1 kqrqkppskpndfhfevfnvpicsnnpntcwaickripnkkpgk 48

RESULT 12
W39220
ID W39220 standard; peptide; 49 AA.
XX
AC W39220;
XX
DT 27-AUG-1998 (first entry)
XX
DE Human RSV A subtype G protein fragment (aa. 149-157) strain A6614.
XX
KW G protein; treatment; prevention; diagnosis; infection; immunity;
KW antibody; Pneumovirus; identification; vaccine; cell receptor.
XX
OS Human respiratory syncytial virus.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 25..38
FT Disulfide-bond 28..34
XX
PN WO9746581-A1.
XX
PD 11-DEC-1997.

```

PI Gorman JU;
XX
XX WPI; 1998-042117/04.
XX
XX Peptide(s) derived from specific region of respiratory syncytial
PT virus G protein - used to treat, prevent, diagnose and immunise
PT against Pneumovirus infection
XX
XX Example 4; Fig 12; 75pp; English.
XX
XX W39244-W39252 are derivatives of the human respiratory syncytial virus
CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments
CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
CC infection and to immunise against such infections. Antibodies raised
CC from these fragments may also be used diagnostically. The fragments may
CC also be used to identify compounds able to inhibit binding of RSV to host
CC cells and for characterisation of cell receptors for Pneumoviruses. When
CC the fragments are used in combination with existing vaccines, they may
CC allow a reduction in dose, and thus side effects, of the vaccine.
XX
XX Sequence 42 AA;

Query Match 85.7%; Score 42; DB 19; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e-36;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 KORONKPPSKPNNDFHFVFNFVPCSCSNNTCWAICKRIP 42
| | | | | | | | | | | | | | | | | | | | | |
Db 1 kqgnkppskpnndfhfvfnfvpvpcscsnntcwaickrip 42

RESULT 14
W97304
ID W97304 standard; Peptide; 43 AA.
AC
XX W97304;
XX
XX 26-MAY-1999 (first entry)
XX
XX Peptide which induces the antibodies of the invention.

XX Antibody; epitope; protein G; respiratory syncytial virus; RSV;
KW RSV-related disease.
XX
XX Synthetic.
OS
XX WO9903987-A2.
PN
XX
XX 28-JAN-1999.
PD
XX
PF 17-JUL-1998; 98WO-FR01570.
XX
XX 17-JUL-1997; 97FR-0009079.
PR
XX
XX (FABR) FABRE MEDICAMENT SA PIERRE.
PA
XX
XX Beck A, Goestch L, Nguyen TN, Power U;
PI
XX
XX WPI; 1999-132232/11.
DR N-PSDB; X15813.
XX
XX New antibodies directed against epitopes in protein G of respiratory
PT syncytial virus - used for treatment, prevention and diagnosis of
PT RSV infections
XX
XX Claim 3; Page 51; 54pp; French.

XX The present sequence represents a peptide which induces the antibodies
CC of the invention. The specification describes mono- or poly-clonal
CC antibodies that are directed against an epitope that corresponds to
CC amino acids 150-159, 176-189, 194-207 or 155-176 of protein G of
CC respiratory syncytial virus (RSV), subgroups A or B. The antibodies

CC are used for treating, preventing (passive or active immunisation)
CC and diagnosing RSV-related diseases, including differentiating between
CC infection by subgroups A or B.
XX
SQ Sequence 43 AA;

Query Match 81.6%; Score 40; DB 20; Length 43;
Best Local Similarity 100.0%; Pred. No. 2.3e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 KPNNDFHFEVFNPCSCSNPTCWAICKRIPNKKPGKK 49
Db 1 kpndfhfevfnfvpicsnnpctcwaickripnkkpgkk 40

RESULT 15

W39218
ID W39218 standard; peptide; 49 AA.
XX
AC W39218;
XX
DT 27-AUG-1998 (first entry)
XX
DE Human RSV A subtype G protein fragment (aa 149-157) strain long A.
XX
KW G protein; treatment; prevention; diagnosis; infection; immunity;
XX antibody; Pneumovirus; identification; vaccine; cell receptor.
XX
OS Human respiratory syncytial virus.

Key Location/Qualifiers

FT Disulfide-bond 25..38
ET Disulfide-bond 28..34

XX WO9746581-A1.

XX 11-DEC-1997.

XX 04-JUN-1997; 97WO-AU00351.

XX 05-JUN-1996; 96AU-0000265.

XX (BIOM-) BIOMOLECULAR RES INST LTD.

XX Gorman JJ;

XX WPI; 1998-042117/04.

PT Peptide(s) derived from specific region of respiratory syncytial
PT virus G protein - used to treat, prevent, diagnose and immunise
PT against Pneumovirus infection

XX Claim 5; Fig 2; 75pp; English.

CC W39217-W39234 are fragments of the human respiratory syncytial virus
(RSV) G protein corresponding to amino acids 149 to 197. These fragments
CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
CC infection and to immunise against such infections. Antibodies raised
CC from these fragments may also be used diagnostically. The fragments may
CC also be used to identify compounds able to inhibit binding of RSV to host
CC cells and for characterisation of cell receptors for Pneumoviruses. When
CC the fragments are used in combination with existing vaccines, they may
CC allow a reduction in dose, and thus side effects, of the vaccine.

XX Sequence 49 AA;

Query Match 81.6%; Score 40; DB 19; Length 49;
Best Local Similarity 100.0%; Pred. No. 2.6e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 KPNNDFHFEVFNPCSCSNPTCWAICKRIPNKKPGKK 49

Db 10 kpndfhfevfnfvpicsnnpctcwaickripnkkpgkk 49

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OM protein - protein search, using sw model

Run on: May 21, 2001, 14:16:32 ; Search time 11.77 Seconds
(without alignments)
79.977 Million cell updates/sec

Title: US-09-202-035-1

Perfect score: 49

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Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 185757 seqs, 19210857 residues

Word size : 0

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	40	81.6	298	2	US-08-838-189D-8
4	40	81.6	298	3	US-08-852-344D-8
5	40	81.6	298	3	US-08-344-639E-8
6	40	81.6	298	4	US-08-467-969A-8
7	40	81.6	298	4	US-08-467-961A-8
8	36	73.5	37	3	US-08-793-792-12
9	32	65.3	32	3	US-08-793-792-8
10	28	57.1	28	3	US-08-793-792-4
11	16	32.7	16	3	US-08-793-792-13
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13	13	26.5	32	3	US-08-793-792-7
14	13	26.5	37	3	US-08-793-792-11
15	12	24.5	30	4	US-08-836-504A-5
16	12	24.5	30	4	US-08-836-504A-6
17	6	12.2	28	2	US-08-451-371-1
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21	6	12.2	28	2	US-08-451-371-5
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24	5	10.2	11	4	US-09-224-785-31
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27	5	10.2	14	4	US-08-836-501-9

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Sequence 20, Appl	US-08-836-501-20	17	4
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Sequence 44, Appl	US-09-282-351A-44	22	4
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Sequence 47, Appl	US-09-282-351A-47	22	4
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Sequence 103, Appl	US-08-836-561-103	127	3
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Sequence 13, Appl	US-08-729-416C-13	164	3
Sequence 33, Appl	US-08-168-091A-33	165	1
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Sequence 4, Appl	PCT-US93-00324-4	220	5
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Sequence 4, Appl	US-07-929-198-4	226	1
Sequence 6, Appl	US-07-929-198-6	226	1
Sequence 15, Appl	US-08-557-146-15	226	2
Sequence 15, Appl	US-09-154-344-15	226	2
Sequence 26, Appl	PCT-US94-01149-26	226	5
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Sequence 22, Appl	US-08-729-416C-22	260	3
Sequence 4, Appl	US-08-808-148-4	281	3

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105	5	10.2	311	4	US-09-008-697A-5	Sequence 5, Appl	178	5	10.2	595	2	US-08-376-843-3	Sequence 3, Appl
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107	5	10.2	319	1	US-08-597-495B-22	Sequence 22, Appl	180	5	10.2	603	2	US-08-687-865A-2	Sequence 2, Appl
108	5	10.2	319	4	US-09-008-697A-6	Sequence 6, Appl	181	5	10.2	604	4	US-08-470-335-227	Sequence 227, App
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111	5	10.2	343	1	US-08-047-413-13	Sequence 13, Appl	184	5	10.2	615	2	US-08-484-101B-38	Sequence 38, Appl
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115	5	10.2	359	4	US-09-008-697A-4	Sequence 4, Appl	188	5	10.2	619	3	US-08-461-145C-4	Sequence 4, Appl
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120	5	10.2	378	2	US-08-401-068-14	Sequence 14, Appl	193	5	10.2	625	5	PCT-US92-04295A-26	Sequence 247, App
121	5	10.2	378	2	US-08-846-338-14	Sequence 14, Appl	194	5	10.2	635	4	US-08-470-335-247	Sequence 28, Appl
122	5	10.2	410	2	US-09-018-628-14	Sequence 14, Appl	195	5	10.2	637	1	US-07-847-743B-28	Sequence 28, Appl
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125	5	10.2	420	1	US-08-456-201-29	Sequence 29, Appl	198	5	10.2	637	5	PCT-US92-04295A-28	Sequence 28, Appl
126	5	10.2	420	2	US-08-456-241-29	Sequence 29, App	199	5	10.2	638	4	US-08-470-335-240	Sequence 240, App
127	5	10.2	420	5	PCT-US92-04295A-29	Sequence 29, App	200	5	10.2	644	4	US-08-470-335-250	Sequence 250, App
128	5	10.2	422	1	US-08-036-555B-170	Sequence 170, App	201	5	10.2	645	1	US-07-847-743B-27	Sequence 27, Appl
129	5	10.2	422	1	US-08-469-569-170	Sequence 170, App	202	5	10.2	645	1	US-08-456-201-27	Sequence 27, Appl
130	5	10.2	422	1	US-08-428-948-3	Sequence 3, Appl	203	5	10.2	645	1	US-08-428-926-4	Sequence 4, Appl
131	5	10.2	422	1	US-08-249-322A-170	Sequence 170, App	204	5	10.2	645	1	US-08-428-927-4	Sequence 4, Appl
132	5	10.2	422	1	US-08-428-927-3	Sequence 3, Appl	205	5	10.2	645	1	US-08-428-298-4	Sequence 4, Appl
133	5	10.2	422	1	US-08-428-298-3	Sequence 3, Appl	206	5	10.2	645	1	US-08-339-517-4	Sequence 4, Appl
134	5	10.2	422	1	US-08-339-517-3	Sequence 3, Appl	207	5	10.2	645	2	US-08-456-241-27	Sequence 27, Appl
135	5	10.2	422	1	US-08-469-526A-170	Sequence 170, App	208	5	10.2	645	3	US-08-753-007A-10	Sequence 10, Appl
136	5	10.2	422	2	US-08-734-591A-170	Sequence 170, App	209	5	10.2	645	4	US-09-398-496-10	Sequence 10, Appl
137	5	10.2	422	2	US-08-469-660-170	Sequence 170, App	210	5	10.2	645	4	US-09-020-880-93	Sequence 93, Appl
138	5	10.2	422	3	US-08-753-007A-9	Sequence 9, Appl	211	5	10.2	645	5	PCT-US92-04295A-27	Sequence 27, Appl
139	5	10.2	422	3	US-08-341-018-72	Sequence 72, Appl	212	5	10.2	647	4	US-08-470-335-243	Sequence 243, App
140	5	10.2	422	4	US-09-398-496-9	Sequence 9, Appl	213	5	10.2	664	2	US-08-852-153-8	Sequence 8, Appl
141	5	10.2	422	4	US-08-470-335-170	Sequence 170, App	214	5	10.2	669	1	US-07-847-743B-8	Sequence 8, Appl
142	5	10.2	422	4	US-08-735-021-170	Sequence 170, App	215	5	10.2	669	1	US-07-847-743B-13	Sequence 13, Appl
143	5	10.2	422	4	US-08-734-664A-170	Sequence 170, App	216	5	10.2	669	1	US-08-456-201-8	Sequence 8, Appl
144	5	10.2	422	5	PCT-US94-05083C-166	Sequence 166, App	217	5	10.2	669	1	US-08-456-201-13	Sequence 13, Appl
145	5	10.2	422	5	PCT-US94-05083C-185	Sequence 185, App	218	5	10.2	669	2	US-08-330-161-11	Sequence 11, Appl
146	5	10.2	422	5	PCT-US95-06846A-170	Sequence 170, App	219	5	10.2	669	2	US-08-456-241-8	Sequence 8, Appl
147	5	10.2	425	4	US-08-470-335-226	Sequence 226, App	220	5	10.2	669	2	US-08-456-241-13	Sequence 13, Appl
148	5	10.2	451	1	US-08-417-330A-12	Sequence 12, Appl	221	5	10.2	669	2	US-08-440-401-11	Sequence 11, Appl
149	5	10.2	456	2	US-09-018-628-16	Sequence 16, Appl	222	5	10.2	669	2	US-08-419-878B-11	Sequence 11, Appl
150	5	10.2	456	2	US-08-910-731-4	Sequence 4, Appl	223	5	10.2	669	5	PCT-US92-04295A-8	Sequence 8, Appl
151	5	10.2	456	2	US-08-795-395-4	Sequence 4, Appl	224	5	10.2	669	5	PCT-US92-04295A-13	Sequence 13, Appl
152	5	10.2	456	3	US-09-273-378-16	Sequence 16, App	225	5	10.2	675	3	US-08-947-965-76	Sequence 76, Appl
153	5	10.2	456	3	US-08-470-335-246	Sequence 246, App	226	5	10.2	677	3	US-08-480-640A-115	Sequence 115, App
154	5	10.2	459	4	US-08-470-335-239	Sequence 239, App	227	5	10.2	677	3	US-08-480-640A-193	Sequence 193, App
155	5	10.2	474	2	US-08-185-828A-12	Sequence 12, Appl	228	5	10.2	677	4	US-08-295-802-115	Sequence 115, App
156	5	10.2	474	2	US-08-185-828A-18	Sequence 18, Appl	229	5	10.2	683	3	US-08-947-965-2	Sequence 2, Appl
157	5	10.2	474	3	US-08-185-828A-24	Sequence 24, Appl	230	5	10.2	685	3	US-08-947-965-74	Sequence 74, Appl
158	5	10.2	474	3	US-08-729-416C-1	Sequence 1, Appl	231	5	10.2	732	1	US-07-847-743B-9	Sequence 9, Appl
159	5	10.2	474	3	US-08-729-416C-11	Sequence 11, Appl	232	5	10.2	732	1	US-08-456-201-9	Sequence 9, Appl
160	5	10.2	474	3	US-08-807-342B-2	Sequence 2, Appl	233	5	10.2	732	2	US-08-456-241-9	Sequence 9, Appl
161	5	10.2	481	4	US-08-943-714-10	Sequence 10, Appl	234	5	10.2	732	5	PCT-US92-04295A-9	Sequence 9, Appl
162	5	10.2	491	1	US-08-360-673-4	Sequence 4, Appl	235	5	10.2	768	3	US-08-891-845-2	Sequence 2, Appl
163	5	10.2	498	5	PCT-US94-01101-2	Sequence 2, Appl	236	5	10.2	777	1	US-08-526-964-3	Sequence 3, Appl
164	5	10.2	500	3	US-09-018-628-18	Sequence 18, App	237	5	10.2	777	2	US-08-946-617-3	Sequence 3, Appl
165	5	10.2	500	3	US-09-273-378-18	Sequence 18, App	238	5	10.2	777	3	US-09-031-857-3	Sequence 3, Appl
166	5	10.2	501	2	US-08-969-630-4	Sequence 4, Appl	239	5	10.2	793	3	US-08-374-077C-4	Sequence 4, Appl
167	5	10.2	501	3	US-08-891-845-10	Sequence 10, Appl	240	5	10.2	793	4	US-08-895-590-4	Sequence 4, Appl
168	5	10.2	502	2	US-08-969-630-2	Sequence 2, Appl	241	5	10.2	798	2	US-07-728-215-30	Sequence 30, Appl
169	5	10.2	529	2	US-08-933-227-4	Sequence 4, Appl	242	5	10.2	818	4	US-08-470-335-234	Sequence 234, App
170	5	10.2	553	3	US-09-083-351-2	Sequence 2, Appl	243	5	10.2	821	4	US-08-470-335-228	Sequence 228, App
171	5	10.2	553	4	US-08-083-352-2	Sequence 2, Appl	244	5	10.2	827	4	US-08-470-335-237	Sequence 237, App
172	5	10.2	577	2	US-08-852-153-4	Sequence 4, Appl	245	5	10.2	830	4	US-08-470-335-231	Sequence 231, App
173	5	10.2	586	6	5256558-2	Patent No. 5256558	246	5	10.2	852	4	US-08-470-335-248	Sequence 248, App

247	5	10.2	855	4	US-08-470-335-241	Sequence 241, App	320	4	8.2	15	2	US-08-436-717-121	Sequence 121, App
248	5	10.2	861	4	US-08-470-335-241	Sequence 251, App	321	4	8.2	15	2	US-08-436-717-140	Sequence 140, App
249	5	10.2	864	4	US-08-470-335-244	Sequence 244, App	322	4	8.2	15	2	US-08-582-298-13	Sequence 13, Appl
250	5	10.2	865	4	US-08-470-335-235	Sequence 235, App	323	4	8.2	15	2	US-08-248-839C-152	Sequence 152, App
251	5	10.2	868	4	US-08-470-335-229	Sequence 229, App	324	4	8.2	15	2	US-08-553-501A-66	Sequence 66, Appl
252	5	10.2	874	4	US-08-470-335-238	Sequence 238, App	325	4	8.2	15	2	US-08-553-501A-70	Sequence 70, Appl
253	5	10.2	877	4	US-08-470-335-232	Sequence 232, App	326	4	8.2	15	2	US-08-687-956A-5	Sequence 5, Appl
254	5	10.2	899	4	US-08-470-335-249	Sequence 249, App	327	4	8.2	15	2	US-08-318-157B-27	Sequence 27, Appl
255	5	10.2	905	4	US-08-470-335-242	Sequence 242, App	328	4	8.2	15	2	US-09-086-201-20	Sequence 20, Appl
256	5	10.2	902	4	US-08-074-658-70	Sequence 70, Appl	329	4	8.2	15	2	US-08-765-783A-88	Sequence 88, Appl
257	5	10.2	908	4	US-08-470-335-252	Sequence 252, App	330	4	8.2	15	2	US-08-470-139-11	Sequence 11, Appl
258	5	10.2	911	4	US-08-470-335-245	Sequence 245, App	331	4	8.2	15	2	US-08-470-139-12	Sequence 12, Appl
259	5	10.2	1027	4	US-08-446-137B-2	Sequence 2, Appl	332	4	8.2	15	4	US-08-649-100-28	Sequence 28, Appl
260	5	10.2	1144	1	US-08-147-812-5	Sequence 12, Appl	333	4	8.2	15	4	US-09-205-231-66	Sequence 66, Appl
261	5	10.2	1144	2	US-08-319-866-12	Sequence 12, Appl	334	4	8.2	15	4	US-09-205-231-70	Sequence 70, Appl
262	5	10.2	1144	4	US-09-123-708-2	Sequence 2, Appl	335	4	8.2	15	4	US-08-569-147-38	Sequence 38, Appl
263	5	10.2	1144	4	US-09-123-62A-2	Sequence 2, Appl	336	4	8.2	15	4	US-08-875-309-15	Sequence 15, Appl
264	5	10.2	1253	1	US-07-920-281C-3	Sequence 3, Appl	337	4	8.2	15	5	PCT-US95-11405-7	Sequence 7, Appl
265	5	10.2	1253	4	US-08-466-277-3	Sequence 3, Appl	338	4	8.2	15	5	PCT-US95-11405-13	Sequence 13, Appl
266	5	10.2	1264	1	US-07-789-915A-6	Sequence 6, Appl	339	4	8.2	16	1	US-07-609-716-6	Sequence 6, Appl
267	5	10.2	1264	1	US-08-005-002C-6	Sequence 6, Appl	340	4	8.2	16	1	US-07-794-288D-40	Sequence 40, Appl
268	5	10.2	1264	1	US-08-487-203A-6	Sequence 6, Appl	341	4	8.2	16	1	US-07-942-245-71	Sequence 71, Appl
269	5	10.2	1732	2	US-08-477-451-14	Sequence 14, Appl	342	4	8.2	16	1	US-07-942-245-72	Sequence 72, Appl
270	5	10.2	1781	2	US-08-477-451-11	Sequence 11, Appl	343	4	8.2	16	1	US-07-942-245-73	Sequence 73, Appl
271	5	10.2	1872	6	5386025-6	Patent No. 5386025	344	4	8.2	16	1	US-07-942-245-74	Sequence 74, Appl
272	5	10.2	1873	1	US-08-435-675B-4	Sequence 4, Appl	345	4	8.2	16	1	US-07-942-245-76	Sequence 76, Appl
273	5	10.2	1873	1	US-08-336-257A-7	Sequence 7, Appl	346	4	8.2	16	1	US-07-942-245-95	Sequence 95, Appl
274	4	8.2	4	1	US-07-694-983-5	Sequence 5, Appl	347	4	8.2	16	1	US-07-942-245-96	Sequence 96, Appl
275	4	8.2	4	1	US-07-945-982-4	Sequence 4, Appl	348	4	8.2	16	1	US-07-942-245-97	Sequence 97, Appl
276	4	8.2	5	1	US-08-372-455-4	Sequence 4, Appl	349	4	8.2	16	1	US-07-942-245-102	Sequence 102, App
277	4	8.2	6	1	US-08-056-200-27	Sequence 27, Appl	350	4	8.2	16	1	US-07-942-245-105	Sequence 105, App
278	4	8.2	6	1	US-08-056-200-80	Sequence 80, Appl	351	4	8.2	16	1	US-07-942-245-117	Sequence 117, App
279	4	8.2	6	2	US-08-800-644-27	Sequence 27, Appl	352	4	8.2	16	1	US-07-942-245-145	Sequence 145, App
280	4	8.2	6	2	US-08-800-644-80	Sequence 80, Appl	353	4	8.2	16	1	US-07-942-245-147	Sequence 147, App
281	4	8.2	6	4	US-08-875-309-9	Sequence 9, Appl	354	4	8.2	16	4	US-08-475-411A-6	Sequence 6, Appl
282	4	8.2	5	5	PCT-US96-00310-9	Sequence 9, Appl	355	4	8.2	16	4	US-08-875-309-16	Sequence 16, Appl
283	4	8.2	7	1	US-08-372-952-5	Sequence 5, Appl	356	4	8.2	16	4	US-09-171-705-24	Sequence 24, Appl
284	4	8.2	7	1	US-08-191-338A-6	Sequence 6, Appl	357	4	8.2	16	4	US-09-171-705-25	Sequence 25, Appl
285	4	8.2	7	4	US-08-875-309-5	Sequence 5, Appl	358	4	8.2	16	4	US-08-602-999A-203	Sequence 203, App
286	4	8.2	7	5	PCT-US96-00310-5	Sequence 5, Appl	359	4	8.2	16	4	US-08-478-029A-6	Sequence 6, Appl
287	4	8.2	7	6	5514590-12	Patent No. 5514590	360	4	8.2	16	5	PCT-US91-09422-28	Sequence 28, Appl
288	4	8.2	8	4	US-08-875-309-10	Sequence 10, Appl	361	4	8.2	16	5	PCT-US95-09261-4	Sequence 4, Appl
289	4	8.2	8	5	PCT-US96-00310-10	Sequence 10, Appl	362	4	8.2	16	6	5219837-1	Patent No. 5219837
290	4	8.2	9	1	US-08-097-830E-24	Sequence 24, Appl	363	4	8.2	17	1	US-07-794-288D-39	Sequence 39, Appl
291	4	8.2	9	2	US-08-456-112B-24	Sequence 24, Appl	364	4	8.2	17	2	US-07-963-538B-21	Sequence 21, Appl
292	4	8.2	9	6	5378464-12	Patent No. 5378464	365	4	8.2	17	3	US-08-331-625A-35	Sequence 35, Appl
293	4	8.2	10	2	US-08-556-597-153	Sequence 153, App	366	4	8.2	17	6	5219837-7	Patent No. 5219837
294	4	8.2	10	3	US-08-925-002-6	Sequence 6, Appl	367	4	8.2	17	6	5219837-9	Patent No. 5219837
295	4	8.2	10	6	5258287-42	Patent No. 5258287	368	4	8.2	18	1	US-07-794-288D-38	Sequence 38, Appl
296	4	8.2	11	1	US-07-666-719-18	Sequence 18, Appl	369	4	8.2	18	2	US-09-017-205-57	Sequence 57, Appl
297	4	8.2	11	4	US-09-224-785-26	Sequence 26, Appl	370	4	8.2	18	2	US-08-640-847C-29	Sequence 29, Appl
298	4	8.2	12	1	US-07-794-288D-44	Sequence 44, Appl	371	4	8.2	18	3	US-08-881-094-9	Sequence 9, Appl
299	4	8.2	12	1	US-08-260-582-66	Sequence 66, Appl	372	4	8.2	18	3	US-08-881-094-10	Sequence 10, Appl
300	4	8.2	12	5	PCT-US95-05471-66	Sequence 66, Appl	373	4	8.2	18	3	US-08-881-094-12	Sequence 12, Appl
301	4	8.2	13	1	US-07-781-254A-20	Sequence 20, Appl	374	4	8.2	18	6	5219837-2	Patent No. 5219837
302	4	8.2	13	1	US-07-794-288D-43	Sequence 43, Appl	375	4	8.2	18	6	5219837-3	Patent No. 5219837
303	4	8.2	13	1	US-08-520-599-4	Sequence 4, Appl	376	4	8.2	18	6	5219837-4	Patent No. 5219837
304	4	8.2	13	1	US-08-290-919-15	Sequence 15, Appl	377	4	8.2	18	6	5219837-5	Patent No. 5219837
305	4	8.2	13	3	US-09-188-579-29	Sequence 29, Appl	378	4	8.2	19	1	US-07-794-288D-37	Sequence 37, Appl
306	4	8.2	13	3	US-09-188-579-35	Sequence 35, Appl	379	4	8.2	19	1	US-07-794-288D-150	Sequence 150, App
307	4	8.2	14	1	US-07-794-288D-42	Sequence 42, Appl	380	4	8.2	19	2	US-08-248-839C-96	Sequence 96, Appl
308	4	8.2	14	2	US-07-963-538B-26	Sequence 26, Appl	381	4	8.2	19	2	US-09-174-060-14	Sequence 14, Appl
309	4	8.2	14	5	PCT-US95-13975-8	Sequence 8, Appl	382	4	8.2	19	3	US-08-338-382-14	Sequence 14, Appl
310	4	8.2	15	1	US-08-080-073-19	Sequence 19, Appl	383	4	8.2	19	3	US-08-467-023-236	Sequence 236, App
311	4	8.2	15	1	US-08-080-073-21	Sequence 21, Appl	384	4	8.2	19	4	US-08-652-877-18	Sequence 18, Appl
312	4	8.2	15	1	US-08-080-073-27	Sequence 27, Appl	385	4	8.2	19	5	PCT-US91-02942-67	Sequence 67, Appl
313	4	8.2	15	1	US-07-946-421-8	Sequence 8, Appl	386	4	8.2	20	1	US-08-205-938A-17	Sequence 17, Appl
314	4	8.2	15	1	US-07-794-288D-41	Sequence 41, Appl	387	4	8.2	20	1	US-07-794-288D-36	Sequence 36, Appl
315	4	8.2	15	1	US-08-423-399B-21	Sequence 21, Appl	388	4	8.2	20	1	US-07-794-288D-142	Sequence 142, App
316	4	8.2	15	1	US-08-582-257-13	Sequence 13, Appl	389	4	8.2	20	1	US-07-794-288D-149	Sequence 149, App
317	4	8.2	15	1	US-08-137-117D-121	Sequence 121, App	390	4	8.2	20	1	US-08-430-273-1	Sequence 1, Appl
318	4	8.2	140	1	US-08-137-117D-140	Sequence 140, App	391	4	8.2	20	1	US-07-678-974D-6	Sequence 6, Appl
319	4	8.2	15	1	US-08-434-705B-20	Sequence 20, Appl	392	4	8.2	20	1	US-07-678-974D-46	Sequence 46, Appl

393	4	8.2	20	2	US-08-480-190-35	Sequence 35, Appl	466	4	8.2	23	3	US-08-810-324-6	Sequence 6, Appl1
394	4	8.2	20	2	US-08-480-190-56	Sequence 56, Appl	467	4	8.2	23	3	US-08-810-324-31	Sequence 31, Appl
395	4	8.2	20	2	US-08-488-379-35	Sequence 35, Appl	468	4	8.2	23	3	US-08-810-324-34	Sequence 34, Appl
396	4	8.2	20	2	US-08-488-379-56	Sequence 56, Appl	469	4	8.2	24	1	US-08-103-445-21	Sequence 21, Appl
397	4	8.2	20	2	US-08-107-676-20	Sequence 20, Appl	470	4	8.2	24	1	US-07-794-288D-32	Sequence 32, Appl
398	4	8.2	20	2	US-08-107-676-21	Sequence 21, Appl	471	4	8.2	24	1	US-07-794-288D-77	Sequence 77, Appl
399	4	8.2	20	2	US-08-945-168-52	Sequence 52, Appl	472	4	8.2	24	1	US-07-794-288D-131	Sequence 131, App
400	4	8.2	20	3	US-08-788-231A-10	Sequence 10, Appl	473	4	8.2	24	1	US-07-794-288D-138	Sequence 138, App
401	4	8.2	20	5	PCT-US93-07545-35	Sequence 35, Appl	474	4	8.2	24	1	US-07-794-288D-145	Sequence 145, App
402	4	8.2	20	5	PCT-US93-07545-56	Sequence 56, Appl	475	4	8.2	24	1	US-08-325-071-30	Sequence 30, Appl
403	4	8.2	20	5	PCT-US95-02626-17	Sequence 17, Appl	476	4	8.2	24	1	US-08-461-690B-21	Sequence 21, Appl
404	4	8.2	21	1	US-07-666-719-8	Sequence 8, Appl1	477	4	8.2	24	1	US-08-244-701B-47	Sequence 47, Appl
405	4	8.2	21	1	US-07-918-953-15	Sequence 15, Appl	478	4	8.2	24	2	US-08-470-775-12	Sequence 12, Appl
406	4	8.2	21	1	US-08-212-696-1	Sequence 1, Appl1	479	4	8.2	24	3	US-09-054-393-5	Sequence 5, Appl1
407	4	8.2	21	1	US-08-158-245-1	Sequence 1, Appl1	480	4	8.2	24	3	US-08-469-318-51	Sequence 51, Appl
408	4	8.2	21	1	US-08-081-661-15	Sequence 15, Appl	481	4	8.2	24	3	US-08-468-609A-51	Sequence 51, Appl
409	4	8.2	21	1	US-08-233-617-1	Sequence 1, Appl1	482	4	8.2	24	3	US-08-192-325B-51	Sequence 51, Appl
410	4	8.2	21	1	US-08-160-376A-1	Sequence 1, Appl1	483	4	8.2	24	3	US-08-559-267A-12	Sequence 12, Appl
411	4	8.2	21	1	US-07-956-700B-18	Sequence 18, Appl	484	4	8.2	24	4	US-08-469-124-12	Sequence 34, Appl
412	4	8.2	21	1	US-08-304-070-1	Sequence 1, Appl1	485	4	8.2	24	4	US-08-847-844A-34	Sequence 34, Appl
413	4	8.2	21	1	US-08-285-661-1	Sequence 1, Appl1	486	4	8.2	24	5	PCT-US95-01185-51	Sequence 51, Appl
414	4	8.2	21	1	US-07-794-288D-35	Sequence 35, Appl	487	4	8.2	25	1	US-08-264-030-6	Sequence 6, Appl1
415	4	8.2	21	1	US-07-794-288D-134	Sequence 134, App	488	4	8.2	25	1	US-08-264-030-7	Sequence 7, Appl1
416	4	8.2	21	1	US-07-794-288D-141	Sequence 141, App	489	4	8.2	25	1	US-08-264-030-8	Sequence 8, Appl1
417	4	8.2	21	1	US-07-794-288D-148	Sequence 148, App	490	4	8.2	25	1	US-08-264-030-11	Sequence 11, Appl
418	4	8.2	21	1	US-08-301-838-1	Sequence 1, Appl1	491	4	8.2	25	1	US-07-794-288D-31	Sequence 31, Appl
419	4	8.2	21	1	US-08-447-925-3	Sequence 3, Appl1	492	4	8.2	25	1	US-07-794-288D-76	Sequence 76, Appl
420	4	8.2	21	1	US-08-389-487-4	Sequence 4, Appl1	493	4	8.2	25	1	US-07-794-288D-130	Sequence 130, App
421	4	8.2	21	1	US-08-389-487-12	Sequence 12, Appl	494	4	8.2	25	1	US-07-794-288D-137	Sequence 137, App
422	4	8.2	21	1	US-08-507-124-2	Sequence 2, Appl1	495	4	8.2	25	1	US-07-794-288D-144	Sequence 144, App
423	4	8.2	21	1	US-08-342-931-1	Sequence 1, Appl1	496	4	8.2	25	1	US-08-416-709-4	Sequence 4, Appl1
424	4	8.2	21	1	US-08-400-256-1	Sequence 1, Appl1	497	4	8.2	25	2	US-08-473-475A-13	Sequence 13, Appl
425	4	8.2	21	1	US-08-476-537-18	Sequence 18, Appl	498	4	8.2	25	4	US-08-974-549A-135	Sequence 135, App
426	4	8.2	21	1	US-08-485-607-18	Sequence 18, Appl	499	4	8.2	26	1	US-07-794-288D-30	Sequence 30, Appl
427	4	8.2	21	2	US-08-508-664-9	Sequence 9, Appl1	500	4	8.2	26	1	US-07-794-288D-75	Sequence 75, Appl
428	4	8.2	21	2	US-08-353-476-85	Sequence 85, Appl	501	4	8.2	26	1	US-07-794-288D-129	Sequence 129, App
429	4	8.2	21	2	US-08-484-219-1	Sequence 1, Appl1	502	4	8.2	26	1	US-07-794-288D-136	Sequence 136, App
430	4	8.2	21	2	US-08-979-587-1	Sequence 1, Appl1	503	4	8.2	26	1	US-07-794-288D-143	Sequence 143, App
431	4	8.2	21	2	US-08-475-879-18	Sequence 18, Appl	504	4	8.2	26	1	US-07-942-245-231	Sequence 231, App
432	4	8.2	21	2	US-08-992-676-1	Sequence 1, Appl1	505	4	8.2	26	1	US-07-942-245-232	Sequence 232, App
433	4	8.2	21	2	US-08-992-676-6	Sequence 6, Appl1	506	4	8.2	26	1	US-07-942-245-233	Sequence 233, App
434	4	8.2	21	2	US-09-134-836-1	Sequence 1, Appl1	507	4	8.2	26	1	US-07-942-245-234	Sequence 234, App
435	4	8.2	21	2	US-09-134-836-7	Sequence 7, Appl1	508	4	8.2	26	1	US-07-942-245-235	Sequence 235, App
436	4	8.2	21	3	US-08-967-867-2	Sequence 2, Appl1	509	4	8.2	26	1	US-07-942-245-236	Sequence 236, App
437	4	8.2	21	3	US-08-651-136C-44	Sequence 44, Appl	510	4	8.2	26	1	US-07-942-245-238	Sequence 238, App
438	4	8.2	21	3	US-08-975-365-1	Sequence 1, Appl1	511	4	8.2	26	1	US-07-942-245-239	Sequence 239, App
439	4	8.2	21	3	US-08-750-391-3	Sequence 3, Appl1	512	4	8.2	26	1	US-07-942-245-240	Sequence 240, App
440	4	8.2	21	3	US-08-788-231A-7	Sequence 7, Appl1	513	4	8.2	26	1	US-07-942-245-241	Sequence 241, App
441	4	8.2	21	6	5164366-3	Patent No. 5164366	514	4	8.2	26	1	US-07-942-245-242	Sequence 242, App
442	4	8.2	21	6	5164366-5	Patent No. 5164366	515	4	8.2	26	1	US-07-942-245-243	Sequence 243, App
443	4	8.2	21	6	5169865-4	Patent No. 5169865	516	4	8.2	26	1	US-07-942-245-248	Sequence 248, App
444	4	8.2	21	6	5514646-2	Patent No. 5514646	517	4	8.2	26	1	US-07-942-245-251	Sequence 251, App
445	4	8.2	21	6	5514646-50	Patent No. 5514646	518	4	8.2	26	1	US-07-942-245-252	Sequence 252, App
446	4	8.2	22	1	US-08-080-073-33	Sequence 33, Appl	519	4	8.2	26	1	US-07-942-245-258	Sequence 258, App
447	4	8.2	22	1	US-08-080-073-34	Sequence 34, Appl	520	4	8.2	26	1	US-07-942-245-261	Sequence 261, App
448	4	8.2	22	1	US-08-080-073-36	Sequence 36, Appl	521	4	8.2	26	1	US-07-942-245-269	Sequence 269, App
449	4	8.2	22	1	US-08-087-831-4	Sequence 4, Appl1	522	4	8.2	26	1	US-07-942-245-270	Sequence 270, App
450	4	8.2	22	1	US-07-794-288D-34	Sequence 34, Appl	523	4	8.2	26	1	US-07-942-245-285	Sequence 285, App
451	4	8.2	22	1	US-07-794-288D-79	Sequence 79, Appl	524	4	8.2	26	1	US-07-942-245-286	Sequence 286, App
452	4	8.2	22	1	US-07-794-288D-133	Sequence 133, App	525	4	8.2	26	1	US-07-942-245-287	Sequence 287, App
453	4	8.2	22	1	US-07-794-288D-140	Sequence 140, App	526	4	8.2	26	1	US-07-942-245-288	Sequence 288, App
454	4	8.2	22	1	US-07-794-288D-147	Sequence 147, App	527	4	8.2	26	1	US-07-942-245-290	Sequence 290, App
455	4	8.2	22	1	US-08-466-945-4	Sequence 4, Appl1	528	4	8.2	26	1	US-07-942-245-291	Sequence 291, App
456	4	8.2	22	2	US-08-248-839C-177	Sequence 177, App	529	4	8.2	26	1	US-07-942-245-292	Sequence 292, App
457	4	8.2	22	6	5204096-8	Patent No. 5204096	530	4	8.2	26	1	US-07-942-245-293	Sequence 293, App
458	4	8.2	23	1	US-07-794-288D-33	Sequence 33, Appl	531	4	8.2	26	1	US-07-942-245-294	Sequence 294, App
459	4	8.2	23	1	US-07-794-288D-78	Sequence 78, Appl	532	4	8.2	26	1	US-07-942-245-295	Sequence 295, App
460	4	8.2	23	1	US-07-794-288D-132	Sequence 132, App	533	4	8.2	26	1	US-07-942-245-296	Sequence 296, App
461	4	8.2	23	1	US-07-794-288D-139	Sequence 139, App	534	4	8.2	26	1	US-07-942-245-297	Sequence 297, App
462	4	8.2	23	1	US-07-794-288D-146	Sequence 146, App	535	4	8.2	26	1	US-07-942-245-298	Sequence 298, App
463	4	8.2	23	3	US-08-746-160-10	Sequence 10, Appl	536	4	8.2	26	1	US-07-942-245-299	Sequence 299, App
464	4	8.2	23	3	US-08-746-160-35	Sequence 35, Appl	537	4	8.2	26	1	US-07-942-245-303	Sequence 303, App
465	4	8.2	23	3	US-08-746-160-38	Sequence 38, Appl	538	4	8.2	26	1	US-07-942-245-304	Sequence 304, App

539	4	8.2	26	1	US-07-942-245-305	Sequence 305, App	612	4	8.2	28	3	US-08-793-792-1	Sequence 1, Appl
540	4	8.2	26	1	US-07-942-245-306	Sequence 306, App	613	4	8.2	28	4	US-08-469-124-13	Sequence 13, Appl
541	4	8.2	26	1	US-07-942-245-312	Sequence 312, App	614	4	8.2	28	5	PCT-US95-01185-52	Sequence 52, Appl
542	4	8.2	26	1	US-07-942-245-315	Sequence 315, App	615	4	8.2	29	1	US-07-794-2880-27	Sequence 27, Appl
543	4	8.2	26	1	US-07-942-245-317	Sequence 317, App	616	4	8.2	29	1	US-07-794-2880-72	Sequence 72, Appl
544	4	8.2	26	1	US-07-942-245-323	Sequence 323, App	617	4	8.2	29	1	US-07-794-2880-94	Sequence 94, Appl
545	4	8.2	26	1	US-07-942-245-324	Sequence 324, App	618	4	8.2	29	1	US-07-794-2880-186	Sequence 186, App
546	4	8.2	26	1	US-07-942-245-325	Sequence 325, App	619	4	8.2	29	1	US-07-794-2880-187	Sequence 187, App
547	4	8.2	26	1	US-07-942-245-326	Sequence 326, App	620	4	8.2	29	1	US-07-794-2880-188	Sequence 188, App
548	4	8.2	26	1	US-07-942-245-327	Sequence 327, App	621	4	8.2	29	1	US-08-471-675A-1	Sequence 1, Appl
549	4	8.2	26	1	US-07-942-245-329	Sequence 329, App	622	4	8.2	30	1	US-07-946-421-11	Sequence 11, Appl
550	4	8.2	26	1	US-07-942-245-330	Sequence 330, App	623	4	8.2	30	1	US-07-794-2880-26	Sequence 26, Appl
551	4	8.2	26	1	US-07-942-245-331	Sequence 331, App	624	4	8.2	30	1	US-07-794-2880-178	Sequence 178, App
552	4	8.2	26	1	US-07-942-245-333	Sequence 333, App	625	4	8.2	30	1	US-07-794-2880-179	Sequence 179, App
553	4	8.2	26	1	US-07-942-245-337	Sequence 337, App	626	4	8.2	30	1	US-07-794-2880-180	Sequence 180, App
554	4	8.2	26	1	US-07-942-245-339	Sequence 339, App	627	4	8.2	30	1	US-07-794-2880-191	Sequence 191, App
555	4	8.2	26	1	US-07-942-245-340	Sequence 340, App	628	4	8.2	30	1	US-07-794-2880-192	Sequence 192, App
556	4	8.2	26	1	US-07-942-245-341	Sequence 341, App	629	4	8.2	30	1	US-07-794-2880-195	Sequence 195, App
557	4	8.2	26	1	US-07-942-245-342	Sequence 342, App	630	4	8.2	30	1	US-07-794-2880-218	Sequence 218, App
558	4	8.2	26	1	US-07-942-245-343	Sequence 343, App	631	4	8.2	30	1	US-07-794-2880-225	Sequence 225, App
559	4	8.2	26	1	US-07-942-245-345	Sequence 345, App	632	4	8.2	30	1	US-08-477-877B-52	Sequence 52, Appl
560	4	8.2	26	1	US-07-942-245-347	Sequence 347, App	633	4	8.2	30	1	US-08-262-037-30	Sequence 30, Appl
561	4	8.2	26	1	US-07-942-245-349	Sequence 349, App	634	4	8.2	30	1	US-08-244-701B-25	Sequence 25, Appl
562	4	8.2	26	1	US-07-942-245-350	Sequence 350, App	635	4	8.2	30	1	US-08-244-701B-26	Sequence 26, Appl
563	4	8.2	26	1	US-07-942-245-351	Sequence 351, App	636	4	8.2	30	1	US-08-137-117D-146	Sequence 146, App
564	4	8.2	26	1	US-07-942-245-353	Sequence 353, App	637	4	8.2	30	1	US-08-137-117D-152	Sequence 152, App
565	4	8.2	26	1	US-07-942-245-355	Sequence 355, App	638	4	8.2	30	1	US-08-137-117D-157	Sequence 157, App
566	4	8.2	26	1	US-07-942-245-356	Sequence 356, App	639	4	8.2	30	2	US-08-472-281A-52	Sequence 52, Appl
567	4	8.2	26	1	US-07-942-245-360	Sequence 360, App	640	4	8.2	30	2	US-08-436-717-146	Sequence 146, App
568	4	8.2	26	1	US-07-942-245-361	Sequence 361, App	641	4	8.2	30	2	US-08-436-717-152	Sequence 152, App
569	4	8.2	26	1	US-07-942-245-365	Sequence 365, App	642	4	8.2	30	2	US-08-436-717-157	Sequence 157, App
570	4	8.2	26	1	US-07-942-245-366	Sequence 366, App	643	4	8.2	30	2	US-08-560-558E-5	Sequence 5, Appl
571	4	8.2	26	1	US-07-942-245-367	Sequence 367, App	644	4	8.2	30	2	US-08-477-989B-52	Sequence 52, Appl
572	4	8.2	26	1	US-07-942-245-368	Sequence 368, App	645	4	8.2	30	4	US-08-649-100-18	Sequence 18, Appl
573	4	8.2	26	1	US-07-942-245-374	Sequence 374, App	646	4	8.2	30	4	US-08-649-100-34	Sequence 34, Appl
574	4	8.2	26	1	US-07-942-245-385	Sequence 385, App	647	4	8.2	30	4	US-08-569-147-54	Sequence 54, Appl
575	4	8.2	26	1	US-07-942-245-458	Sequence 458, App	648	4	8.2	30	4	US-08-569-147-55	Sequence 55, Appl
576	4	8.2	26	1	US-07-942-245-459	Sequence 459, App	649	4	8.2	31	1	US-07-776-272-23	Sequence 23, Appl
577	4	8.2	26	1	US-07-942-245-460	Sequence 460, App	650	4	8.2	31	1	US-08-244-701B-31	Sequence 31, Appl
578	4	8.2	26	1	US-07-942-245-461	Sequence 461, App	651	4	8.2	32	3	US-08-665-259-17	Sequence 17, Appl
579	4	8.2	26	1	US-07-942-245-462	Sequence 462, App	652	4	8.2	32	3	US-08-762-500-17	Sequence 17, Appl
580	4	8.2	26	1	US-07-942-245-463	Sequence 463, App	653	4	8.2	32	3	US-08-793-792-5	Sequence 5, Appl
581	4	8.2	26	1	US-07-942-245-466	Sequence 466, App	654	4	8.2	32	4	US-08-513-968-55	Sequence 55, Appl
582	4	8.2	26	1	US-07-942-245-467	Sequence 467, App	655	4	8.2	32	4	US-08-469-318-191	Sequence 191, App
583	4	8.2	26	1	US-08-487-890A-72	Sequence 72, Appl	656	4	8.2	33	3	US-08-469-318-192	Sequence 192, App
584	4	8.2	26	2	US-08-478-435-72	Sequence 72, Appl	657	4	8.2	33	3	US-08-469-318-193	Sequence 193, App
585	4	8.2	26	2	US-08-337-483-72	Sequence 72, Appl	658	4	8.2	33	3	US-08-468-609A-191	Sequence 191, App
586	4	8.2	26	2	US-08-478-373-72	Sequence 72, Appl	659	4	8.2	33	3	US-08-468-609A-192	Sequence 192, App
587	4	8.2	26	2	US-08-620-151-14	Sequence 14, Appl	660	4	8.2	33	3	US-08-468-609A-193	Sequence 193, App
588	4	8.2	26	3	US-08-474-671-72	Sequence 72, Appl	661	4	8.2	33	5	PCT-US95-01185-191	Sequence 191, App
589	4	8.2	26	3	US-08-483-577A-72	Sequence 72, Appl	662	4	8.2	33	5	PCT-US95-01185-192	Sequence 192, App
590	4	8.2	26	4	US-08-974-549A-57	Sequence 57, Appl	663	4	8.2	33	5	PCT-US95-01185-193	Sequence 193, App
591	4	8.2	27	1	US-08-066-277-1	Sequence 1, Appl	664	4	8.2	35	1	US-08-487-890A-55	Sequence 55, Appl
592	4	8.2	27	1	US-07-794-2880-29	Sequence 29, Appl	665	4	8.2	35	2	US-08-392-625-35	Sequence 35, Appl
593	4	8.2	27	1	US-07-794-2880-74	Sequence 74, Appl	666	4	8.2	35	2	US-08-466-961A-35	Sequence 35, Appl
594	4	8.2	27	1	US-07-794-2880-128	Sequence 128, App	667	4	8.2	35	2	US-08-478-435-55	Sequence 55, Appl
595	4	8.2	27	1	US-07-794-2880-135	Sequence 135, App	668	4	8.2	35	2	US-08-337-483-55	Sequence 55, Appl
596	4	8.2	27	1	US-08-550-815-1	Sequence 1, Appl	669	4	8.2	35	2	US-08-478-373-55	Sequence 55, Appl
597	4	8.2	27	3	US-08-703-089-1	Sequence 2, Appl	670	4	8.2	35	2	US-08-460-890A-45	Sequence 45, Appl
598	4	8.2	28	1	US-08-264-030-2	Sequence 2, Appl	671	4	8.2	35	3	US-08-474-671-55	Sequence 55, Appl
599	4	8.2	28	1	US-08-264-030-3	Sequence 3, Appl	672	4	8.2	35	3	US-08-483-577A-55	Sequence 55, Appl
600	4	8.2	28	1	US-08-264-030-4	Sequence 4, Appl	673	4	8.2	35	3	US-08-167-641C-45	Sequence 45, Appl
601	4	8.2	28	1	US-08-264-030-5	Sequence 5, Appl	674	4	8.2	35	4	US-08-460-971A-45	Sequence 45, Appl
602	4	8.2	28	1	US-08-264-030-10	Sequence 10, Appl	675	4	8.2	35	4	US-08-462-040-45	Sequence 45, Appl
603	4	8.2	28	1	US-07-794-2880-28	Sequence 28, Appl	676	4	8.2	36	1	US-07-882-923-1	Sequence 1, Appl
604	4	8.2	28	1	US-07-794-2880-73	Sequence 73, Appl	677	4	8.2	36	1	US-07-882-923-2	Sequence 2, Appl
605	4	8.2	28	1	US-07-794-2880-127	Sequence 127, App	678	4	8.2	36	1	US-08-264-030-1	Sequence 1, Appl
606	4	8.2	28	2	US-08-470-775-13	Sequence 13, Appl	679	4	8.2	36	1	US-08-338-395-3	Sequence 3, Appl
607	4	8.2	28	3	US-08-859-106A-8	Sequence 8, Appl	680	4	8.2	36	1	US-08-338-395-4	Sequence 4, Appl
608	4	8.2	28	3	US-08-469-318-52	Sequence 52, Appl	681	4	8.2	36	1	US-08-329-151-24	Sequence 24, Appl
609	4	8.2	28	3	US-08-468-609A-52	Sequence 52, App	682	4	8.2	36	1	US-08-487-890A-37	Sequence 37, Appl
610	4	8.2	28	3	US-08-152-325B-52	Sequence 52, Appl	683	4	8.2	36	2	US-08-478-435-37	Sequence 37, Appl
611	4	8.2	28	3	US-08-559-267A-13	Sequence 13, Appl	684	4	8.2	36	2	US-08-337-483-37	Sequence 37, Appl

685	4	8.2	36	2	US-08-478-373-37	Sequence 37, Appl	758	4	8.2	49	1	US-07-662-225A-3	Sequence 3, Appl
686	4	8.2	36	3	US-08-474-671-37	Sequence 37, Appl	759	4	8.2	49	1	US-07-602-847C-22	Sequence 22, Appl
687	4	8.2	36	3	US-08-907-403A-1	Sequence 1, Appl	760	4	8.2	49	1	US-07-965-674-6	Sequence 6, Appl
688	4	8.2	36	3	US-08-907-403A-2	Sequence 2, Appl	761	4	8.2	49	1	US-08-304-051-1	Sequence 1, Appl
689	4	8.2	36	3	US-08-483-577A-37	Sequence 37, Appl	762	4	8.2	49	1	US-08-478-039-87	Sequence 87, Appl
690	4	8.2	36	5	PCT-US95-14303-3	Sequence 3, Appl	763	4	8.2	49	1	US-08-476-349A-87	Sequence 87, Appl
691	4	8.2	36	5	PCT-US95-14303-4	Sequence 4, Appl	764	4	8.2	49	3	US-07-963-538B-3	Sequence 3, Appl
692	4	8.2	37	1	US-07-794-288D-3	Sequence 3, Appl	765	4	8.2	49	3	US-08-995-156A-27	Sequence 27, Appl
693	4	8.2	37	1	US-08-233-389C-8	Sequence 8, Appl	766	4	8.2	49	3	US-08-995-156A-72	Sequence 72, Appl
694	4	8.2	37	1	US-08-233-389C-9	Sequence 9, Appl	767	4	8.2	49	5	PCT-US93-05640-21	Sequence 21, Appl
695	4	8.2	37	2	US-08-801-863-8	Sequence 8, Appl	768	4	8.2	49	5	PCT-US93-05640-6	Sequence 6, Appl
696	4	8.2	37	2	US-08-801-863-9	Sequence 9, Appl	769	4	8.2	49	5	PCT-US93-05640-11	Sequence 11, Appl
697	4	8.2	37	2	US-08-486-956A-8	Sequence 8, Appl	770	4	8.2	50	1	PCT-US95-11445-1	Sequence 32, Appl
698	4	8.2	37	2	US-08-486-956A-9	Sequence 9, Appl	771	4	8.2	50	2	US-08-262-037-32	Sequence 32, Appl
699	4	8.2	37	2	US-09-004-713-8	Sequence 8, Appl	772	4	8.2	50	3	US-07-963-538B-2	Sequence 2, Appl
700	4	8.2	37	2	US-09-004-713-9	Sequence 9, Appl	773	4	8.2	50	3	US-08-995-156A-28	Sequence 28, Appl
701	4	8.2	37	2	US-08-619-841-1	Sequence 1, Appl	774	4	8.2	50	5	US-08-995-156A-73	Sequence 73, Appl
702	4	8.2	37	2	US-08-619-841-2	Sequence 2, Appl	775	4	8.2	50	5	PCT-US91-02942-6	Sequence 6, Appl
703	4	8.2	37	2	US-08-446-929A-1	Sequence 1, Appl	776	4	8.2	50	5	PCT-US91-02942-7	Sequence 7, Appl
704	4	8.2	37	2	US-08-446-929A-2	Sequence 2, Appl	777	4	8.2	50	5	PCT-US91-02942-46	Sequence 46, Appl
705	4	8.2	37	3	US-08-793-792-9	Sequence 9, Appl	778	4	8.2	50	5	PCT-US91-02942-47	Sequence 47, Appl
706	4	8.2	37	6	5424221-4	Sequence 9, Appl	779	4	8.2	50	5	PCT-US91-02942-48	Sequence 48, Appl
707	4	8.2	37	6	5424221-5	Sequence 9, Appl	780	4	8.2	50	5	PCT-US91-02942-49	Sequence 49, Appl
708	4	8.2	38	1	US-07-776-272-19	Sequence 19, Appl	781	4	8.2	50	6	PCT-US91-02942-50	Sequence 50, Appl
709	4	8.2	38	1	US-07-776-272-20	Sequence 20, Appl	782	4	8.2	51	1	US-07-707-542E-1	Sequence 1, Appl
710	4	8.2	38	1	US-07-776-272-21	Sequence 21, Appl	783	4	8.2	51	1	US-07-707-542E-2	Sequence 2, Appl
711	4	8.2	38	1	US-07-776-272-22	Sequence 22, Appl	784	4	8.2	51	1	US-07-707-542E-4	Sequence 4, Appl
712	4	8.2	38	2	US-08-448-481-9	Sequence 9, Appl	785	4	8.2	51	1	US-07-707-542E-5	Sequence 5, Appl
713	4	8.2	38	2	US-08-448-481-9	Sequence 9, Appl	786	4	8.2	51	1	US-07-945-982-1	Sequence 1, Appl
714	4	8.2	38	3	US-08-460-890A-44	Sequence 44, Appl	787	4	8.2	51	1	US-08-372-455-1	Sequence 1, Appl
715	4	8.2	38	3	US-08-167-641C-44	Sequence 44, Appl	788	4	8.2	51	1	US-08-056-200-113	Sequence 113, App
716	4	8.2	38	4	US-08-460-971A-44	Sequence 44, Appl	789	4	8.2	51	1	US-08-472-788A-73	Sequence 73, Appl
717	4	8.2	39	1	US-07-662-225A-4	Sequence 4, Appl	790	4	8.2	51	1	US-08-472-788A-74	Sequence 74, Appl
718	4	8.2	39	1	US-07-662-225A-5	Sequence 5, Appl	791	4	8.2	51	1	US-08-812-025-3	Sequence 3, Appl
719	4	8.2	39	1	US-08-212-236-3	Sequence 3, Appl	792	4	8.2	51	2	US-08-082-842A-73	Sequence 73, Appl
720	4	8.2	39	1	US-08-212-236-4	Sequence 4, Appl	793	4	8.2	51	2	US-08-082-842A-74	Sequence 74, Appl
721	4	8.2	39	3	US-08-258-287B-46	Sequence 46, Appl	794	4	8.2	51	2	US-08-761-248B-14	Sequence 14, Appl
722	4	8.2	39	3	US-08-368-704C-45	Sequence 45, Appl	795	4	8.2	51	2	US-08-800-644-113	Sequence 113, App
723	4	8.2	40	1	US-07-666-719-3	Sequence 3, Appl	796	4	8.2	51	3	US-08-995-156A-29	Sequence 29, Appl
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725	4	8.2	40	1	US-08-645-193B-66	Sequence 66, Appl	798	4	8.2	52	1	US-07-745-206A-28	Sequence 28, Appl
726	4	8.2	40	3	US-08-812-586-39	Sequence 39, Appl	799	4	8.2	52	2	US-08-311-363-28	Sequence 28, Appl
727	4	8.2	40	3	US-08-812-586-40	Sequence 40, Appl	800	4	8.2	52	2	US-08-995-156A-30	Sequence 30, Appl
728	4	8.2	40	3	US-08-477-383-56	Sequence 56, Appl	801	4	8.2	52	3	US-08-995-156A-75	Sequence 75, Appl
729	4	8.2	41	1	US-08-487-174-56	Sequence 56, Appl	802	4	8.2	53	1	US-08-233-617-3	Sequence 3, Appl
730	4	8.2	42	1	US-08-447-925-2	Sequence 2, Appl	803	4	8.2	53	1	US-08-233-617-4	Sequence 4, Appl
731	4	8.2	42	1	US-08-480-750-56	Sequence 56, Appl	804	4	8.2	53	1	US-08-290-919-3	Sequence 3, Appl
732	4	8.2	42	1	US-08-520-599-1	Sequence 1, Appl	805	4	8.2	53	1	US-08-290-919-4	Sequence 4, Appl
733	4	8.2	42	1	US-08-099-334-8	Sequence 8, Appl	806	4	8.2	53	2	US-07-963-538B-1	Sequence 1, Appl
734	4	8.2	42	2	US-08-288-059-34	Sequence 34, Appl	807	4	8.2	53	3	US-08-651-136C-48	Sequence 48, Appl
735	4	8.2	43	2	US-08-499-676A-33	Sequence 33, Appl	808	4	8.2	53	3	US-08-995-156A-31	Sequence 31, Appl
736	4	8.2	44	2	US-08-437-607A-47	Sequence 47, Appl	809	4	8.2	53	3	US-08-995-156A-76	Sequence 76, Appl
737	4	8.2	44	2	US-08-761-248B-8	Sequence 8, Appl	810	4	8.2	53	3	US-09-261-853-2	Sequence 2, Appl
738	4	8.2	45	3	US-08-856-074A-29	Sequence 29, Appl	811	4	8.2	54	3	US-08-995-156A-32	Sequence 32, Appl
739	4	8.2	45	3	US-08-995-156A-23	Sequence 23, Appl	812	4	8.2	54	3	US-08-995-156A-77	Sequence 77, Appl
740	4	8.2	46	2	US-08-511-485-35	Sequence 35, Appl	813	4	8.2	55	1	US-08-262-037-118	Sequence 118, App
741	4	8.2	46	2	US-08-511-485-37	Sequence 37, Appl	814	4	8.2	55	2	US-08-437-607A-49	Sequence 49, Appl
742	4	8.2	46	2	US-08-511-485-38	Sequence 38, Appl	815	4	8.2	55	3	US-08-995-156A-33	Sequence 33, Appl
743	4	8.2	46	2	US-08-613-235-1	Sequence 1, Appl	816	4	8.2	55	3	US-08-995-156A-78	Sequence 78, Appl
744	4	8.2	46	3	US-08-995-156A-24	Sequence 24, Appl	817	4	8.2	56	1	US-08-160-376A-7	Sequence 7, Appl
745	4	8.2	46	3	US-08-995-156A-69	Sequence 69, Appl	818	4	8.2	56	1	US-08-389-487-11	Sequence 11, Appl
746	4	8.2	47	1	US-08-331-394-6	Sequence 6, Appl	819	4	8.2	56	1	US-08-556-823-1	Sequence 1, Appl
747	4	8.2	47	1	US-08-250-858-6	Sequence 6, Appl	820	4	8.2	56	1	US-08-556-823-9	Sequence 9, Appl
748	4	8.2	47	1	US-08-446-915-6	Sequence 6, Appl	821	4	8.2	56	3	US-08-995-156A-34	Sequence 34, Appl
749	4	8.2	47	2	US-08-248-839C-52	Sequence 52, Appl	822	4	8.2	56	3	US-08-995-156A-79	Sequence 79, Appl
750	4	8.2	47	2	US-08-744-139-6	Sequence 6, Appl	823	4	8.2	56	4	US-09-142-469-4	Sequence 4, Appl
751	4	8.2	47	3	US-08-995-156A-25	Sequence 25, Appl	824	4	8.2	56	6	5217896-7	Patent No. 5217896
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753	4	8.2	47	5	PCT-US95-06639-6	Sequence 6, Appl	826	4	8.2	57	3	US-08-995-156A-35	Sequence 35, Appl
754	4	8.2	48	3	US-08-995-156A-26	Sequence 26, Appl	827	4	8.2	57	3	US-08-995-156A-80	Sequence 80, Appl
755	4	8.2	48	3	US-08-995-156A-71	Sequence 71, Appl	828	4	8.2	58	3	US-08-995-156A-36	Sequence 36, Appl
756	4	8.2	49	1	US-07-662-225A-1	Sequence 18, Appl	829	4	8.2	58	3	US-08-995-156A-81	Sequence 81, Appl
757	4	8.2	49	1	US-07-662-225A-2	Sequence 2, Appl	830	4	8.2	59	3	US-08-995-156A-37	Sequence 37, Appl

831	4	8.2	59	3	US-08-995-156A-82	Sequence 82, Appl	904	4	8.2	74	3	US-08-995-156A-97	Sequence 97, Appl
832	4	8.2	60	1	US-07-743-9251-6	Sequence 6, Appl	905	4	8.2	74	3	US-08-743-975-2	Sequence 21, Appl
833	4	8.2	60	1	US-08-447-9251-1	Sequence 1, Appl	906	4	8.2	74	5	PCT-US95-02275-21	Sequence 2, Appl
834	4	8.2	60	1	US-08-099-325-7	Sequence 7, Appl	907	4	8.2	75	3	US-08-995-156A-53	Sequence 53, Appl
835	4	8.2	60	1	US-08-812-025-2	Sequence 2, Appl	908	4	8.2	75	3	US-08-995-156A-98	Sequence 98, Appl
836	4	8.2	60	2	US-08-288-059-33	Sequence 33, Appl	909	4	8.2	76	3	US-08-356-361-28	Sequence 28, Appl
837	4	8.2	60	2	US-08-949-603-10	Sequence 10, Appl	910	4	8.2	76	3	US-08-769-967A-28	Sequence 54, Appl
838	4	8.2	60	2	US-08-706-270A-10	Sequence 10, Appl	911	4	8.2	76	3	US-08-995-156A-54	Sequence 54, Appl
839	4	8.2	60	2	US-08-949-580-10	Sequence 10, Appl	912	4	8.2	76	3	US-08-995-156A-99	Sequence 99, Appl
840	4	8.2	60	2	US-08-950-172A-10	Sequence 10, Appl	913	4	8.2	76	5	PCT-US91-09055-9	Sequence 9, Appl
841	4	8.2	60	2	US-08-968-542C-14	Sequence 14, Appl	914	4	8.2	77	3	US-08-995-156A-55	Sequence 55, Appl
842	4	8.2	60	3	US-08-651-136C-70	Sequence 70, Appl	915	4	8.2	77	3	US-08-995-156A-100	Sequence 100, Appl
843	4	8.2	60	3	US-08-483-503A-1	Sequence 1, Appl	916	4	8.2	78	3	US-08-375-346A-6	Sequence 6, Appl
844	4	8.2	60	3	US-08-483-503A-3	Sequence 3, Appl	917	4	8.2	78	3	US-08-467-123B-6	Sequence 6, Appl
845	4	8.2	60	3	US-08-995-156A-38	Sequence 38, Appl	918	4	8.2	78	3	US-08-995-156A-56	Sequence 56, Appl
846	4	8.2	60	3	US-08-995-156A-83	Sequence 83, Appl	919	4	8.2	78	3	US-08-995-156A-101	Sequence 101, Appl
847	4	8.2	61	1	US-08-262-037-33	Sequence 33, Appl	920	4	8.2	79	1	US-08-665-220-65	Sequence 65, Appl
848	4	8.2	61	2	US-08-744-670-6	Sequence 6, Appl	921	4	8.2	79	2	US-08-499-676A-14	Sequence 14, Appl
849	4	8.2	61	2	US-09-149-933-6	Sequence 6, Appl	922	4	8.2	79	3	US-08-995-156A-57	Sequence 57, Appl
850	4	8.2	61	3	US-08-995-156A-39	Sequence 39, Appl	923	4	8.2	79	3	US-08-995-156A-102	Sequence 102, Appl
851	4	8.2	61	3	US-08-995-156A-84	Sequence 84, Appl	924	4	8.2	80	1	US-08-137-880-41	Sequence 41, Appl
852	4	8.2	62	1	US-08-383-761-11	Sequence 11, Appl	925	4	8.2	80	1	US-08-477-383-41	Sequence 41, Appl
853	4	8.2	62	1	US-08-702-080-5	Sequence 5, Appl	926	4	8.2	80	1	US-08-487-174-41	Sequence 41, Appl
854	4	8.2	62	1	US-08-824-277-11	Sequence 11, Appl	927	4	8.2	80	1	US-08-480-750-41	Sequence 41, Appl
855	4	8.2	62	2	US-08-556-823-8	Sequence 8, Appl	928	4	8.2	80	2	US-08-553-501A-85	Sequence 85, Appl
856	4	8.2	62	2	US-08-913-050A-8	Sequence 8, Appl	929	4	8.2	80	2	US-08-765-783A-104	Sequence 104, Appl
857	4	8.2	62	2	US-08-858-830-5	Sequence 5, Appl	930	4	8.2	80	3	US-08-554-840-12	Sequence 12, Appl
858	4	8.2	62	2	US-08-858-834-5	Sequence 5, Appl	931	4	8.2	80	3	US-08-995-156A-58	Sequence 58, Appl
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861	4	8.2	63	1	US-08-160-376A-6	Sequence 6, Appl	934	4	8.2	81	3	US-08-995-156A-59	Sequence 59, Appl
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864	4	8.2	63	3	US-08-995-156A-86	Sequence 86, Appl	937	4	8.2	82	3	US-08-995-156A-60	Sequence 60, Appl
865	4	8.2	64	1	US-08-372-723-2	Sequence 2, Appl	938	4	8.2	82	3	US-08-995-156A-105	Sequence 105, Appl
866	4	8.2	64	2	US-08-765-179B-10	Sequence 10, Appl	939	4	8.2	83	2	US-08-726-366A-76	Sequence 76, Appl
867	4	8.2	64	3	US-08-995-156A-42	Sequence 42, Appl	940	4	8.2	83	3	US-08-995-156A-61	Sequence 61, Appl
868	4	8.2	64	3	US-08-995-156A-87	Sequence 87, Appl	941	4	8.2	83	3	US-08-995-156A-106	Sequence 106, Appl
869	4	8.2	65	1	US-08-468-674B-71	Sequence 71, Appl	942	4	8.2	83	3	US-08-875-811-2	Sequence 2, Appl
870	4	8.2	65	1	US-08-780-571-71	Sequence 71, Appl	943	4	8.2	83	4	US-07-791-931-3	Sequence 3, Appl
871	4	8.2	65	3	US-08-995-156A-43	Sequence 43, Appl	944	4	8.2	84	3	US-08-995-156A-62	Sequence 62, Appl
872	4	8.2	65	3	US-08-995-156A-88	Sequence 88, Appl	945	4	8.2	84	3	US-08-995-156A-107	Sequence 107, Appl
873	4	8.2	65	5	PCT-US91-01840-7	Sequence 7, Appl	946	4	8.2	85	3	US-08-995-156A-63	Sequence 63, Appl
874	4	8.2	66	1	US-08-291-060B-5	Sequence 5, Appl	947	4	8.2	85	3	US-08-995-156A-108	Sequence 108, Appl
875	4	8.2	66	3	US-08-995-156A-44	Sequence 44, Appl	948	4	8.2	86	1	US-07-715-183C-1	Sequence 1, Appl
876	4	8.2	66	3	US-08-995-156A-89	Sequence 89, Appl	949	4	8.2	86	1	US-08-497-312-27	Sequence 27, Appl
877	4	8.2	67	3	US-08-995-156A-45	Sequence 45, Appl	950	4	8.2	86	2	US-08-465-380-45	Sequence 45, Appl
878	4	8.2	67	3	US-08-995-156A-90	Sequence 90, Appl	951	4	8.2	86	2	US-08-465-380-46	Sequence 46, Appl
879	4	8.2	68	3	US-08-995-156A-46	Sequence 46, Appl	952	4	8.2	86	2	US-08-486-397-45	Sequence 45, Appl
880	4	8.2	68	3	US-08-995-156A-91	Sequence 91, Appl	953	4	8.2	86	2	US-08-486-397-46	Sequence 46, Appl
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888	4	8.2	69	5	PCT-US95-02275-17	Sequence 17, Appl	961	4	8.2	86	3	US-08-995-156A-109	Sequence 109, Appl
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894	4	8.2	72	3	US-08-995-156A-50	Sequence 50, Appl	967	4	8.2	86	3	US-09-249-451-46	Sequence 46, Appl
895	4	8.2	72	3	US-08-995-156A-95	Sequence 95, Appl	968	4	8.2	86	3	US-08-809-455-45	Sequence 45, Appl
896	4	8.2	73	3	US-08-995-156A-51	Sequence 51, Appl	969	4	8.2	86	3	US-08-809-455-46	Sequence 46, Appl
897	4	8.2	73	3	US-08-995-156A-96	Sequence 96, Appl	970	4	8.2	86	3	US-09-249-461-45	Sequence 45, Appl
898	4	8.2	74	1	US-08-543-238-2	Sequence 2, Appl	971	4	8.2	86	3	US-09-249-461-46	Sequence 46, Appl
899	4	8.2	74	1	US-08-420-526-2	Sequence 2, Appl	972	4	8.2	86	4	US-09-249-448-45	Sequence 45, Appl
900	4	8.2	74	1	US-08-280-443-21	Sequence 21, Appl	973	4	8.2	86	4	US-09-249-448-46	Sequence 46, Appl
901	4	8.2	74	1	US-08-457-459-21	Sequence 21, Appl	974	4	8.2	87	1	US-08-497-312-16	Sequence 16, Appl
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979 | 4 | 8.2 | 87 | 2 | US-08-634-641-44 | Sequence 44, Appl
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998 | 4 | 8.2 | 88 | 3 | US-08-809-455-43 | Sequence 43, Appl
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ALIGNMENTS

RESULT 1
5194595-19
; Patent No. 5194595
; APPLICANT: WATHEN, MICHAEL W.
; TITLE OF INVENTION: CHIMERIC GLYCOPROTEINS CONTAINING
; IMMUNOGENIC SEGMENT OF THE GLYCOPROTEINS OF HUMAN RESPIRATORY
; SYNCYTIAL VIRUS
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/543,780
; FILING DATE: 31-OCT-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 137,387
; FILING DATE: 23-DEC-1987
; SEQ ID NO:19:
; LENGTH: 681
5194595-19

Query Match 100.0%; Score 49; DB 6; Length 681;
Best Local Similarity 100.0%; Pred. No. 6.3e-43;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KORONKPPSPKNDHFVFNPCSCSNNTCWAICKRIPNKKPGKK 49
Db 543 KORONKPPSPKNDHFVFNPCSCSNNTCWAICKRIPNKKPGKK 591

RESULT 2
US-08-467-963C-8
; Sequence 8, Application US/08467963C
; Patent No. 5968776
; GENERAL INFORMATION:
; APPLICANT: KLEIN, Michel H
; APPLICANT: DU, Run-Pan
; APPLICANT: EWASYSHYN, Mary E
; TITLE OF INVENTION: MULTIMERIC HYBRID GENE ENCODING A
; TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST
; TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto

; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,963C
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/838,189
; FILING DATE: 16-APR-1997
; APPLICATION NUMBER: US 08/001,554
; FILING DATE: 06-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9200117.1
; FILING DATE: 06-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-474 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 298 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-467-963C-8

Query Match 81.6%; Score 40; DB 2; Length 298;
Best Local Similarity 100.0%; Pred. No. 5.6e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KPNDHFVFNPCSCSNNTCWAICKRIPNKKPGKK 49
Db 158 KPNDHFVFNPCSCSNNTCWAICKRIPNKKPGKK 197

RESULT 3
US-08-838-189D-8
; Sequence 8, Application US/08838189D
; Patent No. 5998169
; GENERAL INFORMATION:
; APPLICANT: KLEIN, Michel H
; APPLICANT: DU, Run-Pan
; APPLICANT: EWASYSHYN, Mary E
; TITLE OF INVENTION: MULTIMERIC HYBRID GENE ENCODING A
; TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST
; TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,189D
; FILING DATE: 16-APR-1997
; CLASSIFICATION: 435

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;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/001,554
; FILING DATE: 06-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9200117.1
; FILING DATE: 06-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-687 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 298 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-838-189D-8

Query Match 81.6%; Score 40; DB 2; Length 298;
Best Local Similarity 100.0%; Pred. No. 5.6e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KPNDHFHFVFNPCSCSNNPTCWAICKRIPNKKPGKK 49
|||||
Db 158 KPNDHFHFVFNPCSCSNNPTCWAICKRIPNKKPGKK 197
|||||

RESULT 4
US-08-852-344D-8
; Sequence 8, Application US/08852344D
; Patent No. 6017539
; GENERAL INFORMATION:
; APPLICANT: KLEIN, Michel H
; APPLICANT: DU, Run-Pan
; APPLICANT: EWASYSHYN, Mary E
; TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION
; TITLE OF INVENTION: AGAINST PARAINFLUENZA VIRUS AND RESPIRATORY
; TITLE OF INVENTION: SYNCYTIAL VIRUS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,344D
; FILING DATE: 07-MAY-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,639
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-688 MIS:jb
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 298 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-08-344-639E-8

Query Match 81.6%; Score 40; DB 3; Length 298;
Best Local Similarity 100.0%; Pred. No. 5.6e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KPNDHFHFVFNPCSCSNNPTCWAICKRIPNKKPGKK 49
|||||
Db 158 KPNDHFHFVFNPCSCSNNPTCWAICKRIPNKKPGKK 197
|||||

RESULT 5
US-08-344-639E-8
; Sequence 8, Application US/08344639E
; Patent No. 6033668
; GENERAL INFORMATION:
; APPLICANT: Klein, Michel H
; APPLICANT: Du, Run-Pan
; APPLICANT: Ewasysyn, Mary E
; TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS
; TITLE OF INVENTION: PROTECTION AGAINST PARAINFLUENZA VIRUS
; TITLE OF INVENTION: AND RESPIRATORY SYNCYTIAL VIRUS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 330 University Avenue, 6th Floor
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,639E
; FILING DATE: 14-NOV-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/001,554
; FILING DATE: 06-JAN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9200117.1
; FILING DATE: 06-JAN-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-391 MIS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; TELEFAX: 065-24567 SIMBAS
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 298 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-08-344-639E-8

Query Match 81.6%; Score 40; DB 3; Length 298;
Best Local Similarity 100.0%; Pred. No. 5.6e-34;
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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 298 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-852-344D-8

Query Match 81.6%; Score 40; DB 3; Length 298;
Best Local Similarity 100.0%; Pred. No. 5.6e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KPNDHFHFVFNPCSCSNNPTCWAICKRIPNKKPGKK 49
|||||
Db 158 KPNDHFHFVFNPCSCSNNPTCWAICKRIPNKKPGKK 197
|||||

RESULT 5
US-08-344-639E-8
; Sequence 8, Application US/08344639E
; Patent No. 6033668
; GENERAL INFORMATION:
; APPLICANT: Klein, Michel H
; APPLICANT: Du, Run-Pan
; APPLICANT: Ewasysyn, Mary E
; TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS
; TITLE OF INVENTION: PROTECTION AGAINST PARAINFLUENZA VIRUS
; TITLE OF INVENTION: AND RESPIRATORY SYNCYTIAL VIRUS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 330 University Avenue, 6th Floor
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,639E
; FILING DATE: 14-NOV-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/001,554
; FILING DATE: 06-JAN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9200117.1
; FILING DATE: 06-JAN-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-391 MIS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; TELEFAX: 065-24567 SIMBAS
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 298 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-08-344-639E-8

Query Match 81.6%; Score 40; DB 3; Length 298;
Best Local Similarity 100.0%; Pred. No. 5.6e-34;
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; FILING DATE:
; CLASSIFICATION: 514
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
US-08-793-792-12

Query Match 73.5%; Score 36; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.3e-30;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KPNDHFHEVFNVPSCSNNPTCWAICKRI 45
Db 2 KPNDHFHEVFNVPSCSNNPTCWAICKRI 37

RESULT 9
US-08-793-792-8
; Sequence 8, Application US/08793792
; Patent No. 6077511
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Antigenic peptides derived from the

; TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis
; TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.
; NUMBER OF SEQUENCES: 13
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION NUMBER: US/08/793,792
; FILING DATE:
; CLASSIFICATION: 514
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
US-08-793-792-8

Query Match 65.3%; Score 32; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.5e-26;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KPNDHFHEVFNVPSCSNNPTCWAICKRI 41
Db 1 KPNDHFHEVFNVPSCSNNPTCWAICKRI 32

RESULT 10
US-08-793-792-4
; Sequence 4, Application US/08793792
; Patent No. 6077511
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Antigenic peptides derived from the

; TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis
; TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.
; NUMBER OF SEQUENCES: 13
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,792
; FILING DATE:
; CLASSIFICATION: 514
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
US-08-793-792-4

Query Match 57.1%; Score 28; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.7e-22;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PNNDHFHEVFNVPSCSNNPTCWAIC 38
Db 1 PNNDHFHEVFNVPSCSNNPTCWAIC 28

RESULT 11
US-08-793-792-13
; Sequence 13, Application US/08793792
; Patent No. 6077511
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Antigenic peptides derived from the

; TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis
; TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.
; NUMBER OF SEQUENCES: 13
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,792
; FILING DATE:
; CLASSIFICATION: 514
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
US-08-793-792-13

Query Match 32.7%; Score 16; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 SICSNPTCWAICKRI 41
Db 1 SICSNPTCWAICKRI 16

RESULT 12
US-08-793-792-3
; Sequence 3, Application US/08793792
; Patent No. 6077511
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Antigenic peptides derived from the

;; TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis
;; TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.
;; NUMBER OF SEQUENCES: 13
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/793,792
;; FILING DATE:
;; CLASSIFICATION: 514
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 28 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
US-08-793-792-3

Query Match 26.5%; Score 13; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 HFEVFNVPSCIC 28
| | | | | | | | | |
Db 6 HFEVFNVPSCIC 18

RESULT 13
US-08-793-792-7
;; Sequence 7, Application US/08793792
;; Patent No. 6077511
;; GENERAL INFORMATION:
;; APPLICANT:
;; TITLE OF INVENTION: Antigenic peptides derived from the
;; TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis
;; TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.
;; NUMBER OF SEQUENCES: 13
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/793,792
;; FILING DATE:
;; CLASSIFICATION: 514
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 32 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
US-08-793-792-7

Query Match 26.5%; Score 13; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.6e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 HFEVFNVPSCIC 28
| | | | | | | | | |
Db 7 HFEVFNVPSCIC 19

RESULT 14
US-08-793-792-11

;; Sequence 11, Application US/08793792
;; Patent No. 6077511
;; GENERAL INFORMATION:
;; APPLICANT:
;; TITLE OF INVENTION: Antigenic peptides derived from the
;; TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis
;; TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.
;; NUMBER OF SEQUENCES: 13
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/793,792
;; FILING DATE:
;; CLASSIFICATION: 514
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 37 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
US-08-793-792-11

Query Match 26.5%; Score 13; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 HFEVFNVPSCIC 28
| | | | | | | | | |
Db 8 HFEVFNVPSCIC 20

RESULT 15
US-08-836-504A-5
;; Sequence 5, Application US/08836504A
;; Patent No. 6130091
;; GENERAL INFORMATION:
;; APPLICANT: Binz, Hans
;; APPLICANT: Nguyen Ngoc, Thien
;; APPLICANT: Stahl, Stefan
;; APPLICANT: Uhlen, Mathias
;; APPLICANT: Nygren, Per Ake
;; TITLE OF INVENTION: Method for obtaining a peptide derived
;; TITLE OF INVENTION: from the respiratory syncytial virus, polypeptide and
;; TITLE OF INVENTION: bacteria expressing it, and their applications as
;; NUMBER OF SEQUENCES: 11
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Rockey, Milnamow & Katz
;; STREET: 180 N. Stetson Avenue, 2 Prudential Plaza,
;; CITY: Chicago
;; STATE: IL
;; COUNTRY: USA
;; ZIP: 60601
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/836,504A
;; FILING DATE: 07-MAY-1997
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Katz, Martin L.
;; REGISTRATION NUMBER: 25,011
;; REFERENCE/DOCKET NUMBER: PIE1514P0200US

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-836-504A-5

Query Match 24.5%; Score 12; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 SICSNPTCWA 37
Db 15 SICSNPTCWA 26

Search completed: May 21, 2001, 14:17:54
Job time: 82 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 21, 2001, 14:16:42 ; Search time 13.03 Seconds
(without alignments)
258.436 Million cell updates/sec

Title: US-09-202-035-1

Perfect score: 49

Sequence: 1 KORQNKPPSKPNDFEYF.....NNPTCWAICKRIPNKKPGKK 49

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Gapop 60.0 , Gapext 60.0

Searched: 198801 seqs, 68722935 residues

Word size : 0

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

PIR_67.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	298	1	MGNZ
2	48	98.0	297	2	JQ1205
3	48	98.0	297	2	JQ1204
4	40	81.6	297	2	JQ1208
5	40	81.6	297	2	JQ1206
6	40	81.6	298	1	MGNZRL
7	40	81.6	298	2	JC5680
8	35	71.4	297	2	JQ1209
9	33	67.3	298	2	JQ1207
10	13	26.5	292	1	MGNZ18
11	13	26.5	292	1	MGNZ60
12	7	14.3	1255	1	B44213
13	7	14.3	1468	2	T05672
14	6	12.2	23	2	D34047
15	6	12.2	92	2	S69116
16	6	12.2	94	2	T20064
17	6	12.2	126	2	T35556
18	6	12.2	159	2	S44915
19	6	12.2	191	2	T01264
20	6	12.2	196	2	JQ1078
21	6	12.2	196	2	PD0004
22	6	12.2	205	2	T34205
23	6	12.2	206	2	A71019
24	6	12.2	212	2	S73466
25	6	12.2	218	2	A64201
26	6	12.2	219	2	S42674
27	6	12.2	229	2	T27466
28	6	12.2	244	2	S27914
29	6	12.2	278	2	S46017

30	12.2	301	2	S62459	hypothetical prote
31	6	317	2	T32857	hypothetical prote
32	6	342	2	T25637	hypothetical prote
33	6	363	2	S67247	hypothetical prote
34	6	370	2	H64545	lipopolysaccharide
35	6	444	2	S05313	fibrinogen gamma-B
36	6	451	2	S33612	isocitrate dehydro
37	6	508	2	A29605	protein A precursor
38	6	524	1	QVSAA	probable phenylala
39	6	544	2	S75388	hypothetical prote
40	6	614	2	T19963	cytochrome-c oxida
41	6	616	2	JX0140	potassium channel
42	6	625	2	S13919	DNA repair protein
43	6	631	2	A54659	type III DNA modif
44	6	641	2	F71810	hypothetical prote
45	6	740	2	T22638	hypothetical prote
46	6	1199	2	T33337	hypothetical prote
47	6	1232	2	T05342	hypothetical prote
48	6	1249	2	A56511	myosin I myoA - Em
49	6	1254	1	VHWVVE	structural polypro
50	6	1254	1	VHWVVT	structural polypro
51	6	1254	1	JQ1978	structural polypro
52	6	1254	1	JQ1979	structural polypro
53	6	1255	1	B44213	structural polypro
54	6	1261	2	S75130	sensory transducti
55	6	1273	2	T38292	hypothetical prote
56	6	1277	2	T30532	neural cell adhesi
57	6	1277	2	B43081	vitellogenin vit-6
58	6	1286	1	RNFF2L	DNA-directed RNA p
59	5	10.2	21	F00145	glucan endo-1,3-be
60	5	10.2	25	A48363	2-hydroxyglutaryl-
61	5	10.2	49	B81933	hypothetical prote
62	5	10.2	53	S56728	calcium-dependent
63	5	10.2	61	C70245	hypothetical prote
64	5	10.2	65	S77542	hypothetical prote
65	5	10.2	74	S00302	sok protein - Esch
66	5	10.2	75	Q0BE36	BSLF1 protein - hu
67	5	10.2	84	C81037	hypothetical prote
68	5	10.2	96	A37236	I-309 protein prec
69	5	10.2	101	A71902	hypothetical prote
70	5	10.2	101	T160918	brain factor-3 - r
71	5	10.2	103	C72718	hypothetical prote
72	5	10.2	105	T26718	hypothetical prote
73	5	10.2	106	S51626	FRAC-3 protein -
74	5	10.2	108	S31977	Ig kappa chain - h
75	5	10.2	108	B48924	forkhead transcrip
76	5	10.2	109	S31998	Ig kappa chain - h
77	5	10.2	111	E56556	fork head homolog
78	5	10.2	112	D49846	spal3 protein - Sh
79	5	10.2	117	T49674	forkhead transcrip
80	5	10.2	121	B39926	hypothetical prote
81	5	10.2	121	B48343	hypothetical 13K p
82	5	10.2	123	S18470	wnt protein homolo
83	5	10.2	123	S54857	small nuclear ribo
84	5	10.2	124	C48234	hypothetical prote
85	5	10.2	124	C75433	hypothetical prote
86	5	10.2	126	B42294	holo-[acyl-carrier
87	5	10.2	132	T27247	hypothetical prote
88	5	10.2	136	JU0044	hypothetical 15.8K
89	5	10.2	139	T46457	NADH dehydrogenase
90	5	10.2	141	T11270	hypothetical prote
91	5	10.2	142	T28834	30S ribosomal prot
92	5	10.2	143	T46122	hypothetical prote
93	5	10.2	144	B64516	hypothetical prote
94	5	10.2	146	D84083	nitrogen fixation
95	5	10.2	147	E70019	iron-sulfur cofact
96	5	10.2	151	S71430	DNA repair protein
97	5	10.2	152	S27791	hypothetical prote
98	5	10.2	155	T33305	hypothetical prote
99	5	10.2	155	S25846	homeotic protein H
100	5	10.2	158	S53572	probable membrane
101	5	10.2	158	T27757	hypothetical prote
102	5	10.2	159	S16577	ribosomal protein

103	5	10.2	159	2	T23149	hypothetical prote	176	5	10.2	239	2	T20515	hypothetical prote
104	5	10.2	162	2	D38257	glucan endo-1,3-be	177	5	10.2	240	2	S77884	hypothetical prote
105	5	10.2	162	2	E38257	glucan endo-1,3-be	178	5	10.2	241	2	D43273	hergulin precurs
106	5	10.2	166	2	E71040	hypothetical prote	179	5	10.2	242	2	H1883	hydrogenase expres
107	5	10.2	167	2	I50487	ubiquinol--cytochr	180	5	10.2	242	2	D64632	hydrogenase expres
108	5	10.2	167	2	F70478	hypothetical prote	181	5	10.2	243	2	JC4585	GTP cyclohydrolase
109	5	10.2	169	2	T47558	hypothetical prote	182	5	10.2	243	2	T34680	hypothetical prote
110	5	10.2	171	2	D75174	hypothetical prote	183	5	10.2	244	2	T49893	glycine-rich prote
111	5	10.2	173	2	S47171	gene PR-1 protein	184	5	10.2	246	2	S35620	ribosomal protein
112	5	10.2	175	2	I38408	neu differentiation	185	5	10.2	247	1	KHUCM	chymase (EC 3.4.21
113	5	10.2	175	2	D83304	conserved hypothet	186	5	10.2	248	2	S49323	chymotrypsin (EC 3
114	5	10.2	177	2	T12717	hypothetical prote	187	5	10.2	248	2	T41608	hypothetical prote
115	5	10.2	178	2	T09585	high mobility grou	188	5	10.2	249	1	A35842	chymase (EC 3.4.21
116	5	10.2	178	2	T09584	high mobility grou	189	5	10.2	250	2	S74495	hypothetical prote
117	5	10.2	178	2	E81151	conserved hypothet	190	5	10.2	251	2	S27910	coat protein - gar
118	5	10.2	179	2	I40754	GTP cyclohydrolase	191	5	10.2	251	2	JQ2173	viral coat 27.6K p
119	5	10.2	181	2	T48558	hypothetical prote	192	5	10.2	253	2	S33820	secretory protein
120	5	10.2	182	2	E69401	phenylacrylic acid	193	5	10.2	253	2	C36808	hypothetical prote
121	5	10.2	190	2	A81438	GTP cyclohydrolase	194	5	10.2	254	2	A64437	hypothetical prote
122	5	10.2	191	2	E36889	probable 3-isoprop	195	5	10.2	259	2	T45841	6-phosphogluconol
123	5	10.2	191	2	A81870	hypothetical prote	196	5	10.2	259	2	C82153	probable PTS syste
124	5	10.2	191	2	T17995	hypothetical prote	197	5	10.2	260	2	A71949	nh(3)-dependent na
125	5	10.2	194	2	T15927	hypothetical prote	198	5	10.2	260	2	A64561	NH(3)-dependent NA
126	5	10.2	196	2	S50487	hypothetical prote	199	5	10.2	262	2	T22371	hypothetical prote
127	5	10.2	199	2	T29943	hypothetical prote	200	5	10.2	265	2	T42419	hypothetical prote
128	5	10.2	200	2	T07149	systemin precursor	201	5	10.2	265	2	T40259	hypothetical prote
129	5	10.2	201	2	B72380	hypothetical prote	202	5	10.2	269	2	T18145	hypothetical prote
130	5	10.2	201	2	A64737	yadL protein - Esc	203	5	10.2	269	2	S74024	hypothetical prote
131	5	10.2	201	2	T49309	hypothetical prote	204	5	10.2	273	1	EDBE12	immediate-early pr
132	5	10.2	202	2	T34287	hypothetical prote	205	5	10.2	273	2	F71645	hypothetical prote
133	5	10.2	203	2	A49647	GTP-binding protei	206	5	10.2	273	2	T40611	hypothetical prote
134	5	10.2	203	2	T48129	hypothetical prote	207	5	10.2	273	2	T33424	hypothetical prote
135	5	10.2	205	2	I46876	phosphoprotein pho	208	5	10.2	274	2	E81319	probable glucosylt
136	5	10.2	206	2	T06852	hypothetical prote	209	5	10.2	274	2	S69561	hypothetical prote
137	5	10.2	209	1	S48459	probable dual spec	210	5	10.2	275	2	A69413	conserved hypothet
138	5	10.2	211	2	D50111	hypothetical prote	211	5	10.2	276	2	T38825	hypothetical prote
139	5	10.2	213	2	S29924	cyclin 1 - alfalfa	212	5	10.2	278	2	S16678	Lyl-1 protein - mo
140	5	10.2	214	2	S74854	hypothetical prote	213	5	10.2	279	2	B72255	dimethyladenosine
141	5	10.2	214	2	B70470	hypothetical prote	214	5	10.2	279	2	C70458	diaminopelmate ep
142	5	10.2	215	2	T22446	hypothetical prote	215	5	10.2	279	2	T16736	hypothetical prote
143	5	10.2	216	2	H82608	transcription regu	216	5	10.2	281	1	B47629	cell surface glyco
144	5	10.2	218	1	HSC11	histone H1.02 - ch	217	5	10.2	282	2	G64479	hypothetical prote
145	5	10.2	218	2	A23055	histone H1.01 - ch	218	5	10.2	284	2	T42608	immediate-early pr
146	5	10.2	218	2	S01262	histone H1 - musco	219	5	10.2	285	2	A34469	envelope protein p
147	5	10.2	219	2	C65074	hypothetical prote	220	5	10.2	285	2	B82459	hypothetical prote
148	5	10.2	220	2	I50588	fibroblast growth	221	5	10.2	286	2	S07193	chorion protein s3
149	5	10.2	220	2	E71857	probable outer mem	222	5	10.2	286	2	T24233	hypothetical prote
150	5	10.2	223	2	T21669	hypothetical prote	223	5	10.2	288	2	B45580	transcription fact
151	5	10.2	223	2	H65165	hypothetical 22.0	224	5	10.2	288	2	S26028	NADH dehydrogenase
152	5	10.2	223	2	D69311	conserved hypothet	225	5	10.2	290	2	T34572	5,10-methylenetet
153	5	10.2	224	2	JN0798	restriction endonu	226	5	10.2	292	1	H64123	hypothetical prote
154	5	10.2	225	1	A25910	small nuclear ribo	227	5	10.2	292	2	S52888	hypothetical prote
155	5	10.2	225	2	S66212	triose-phosphate i	228	5	10.2	293	2	S09209	SUB1 protein - yea
156	5	10.2	226	2	F82052	phosphoglycolate p	229	5	10.2	294	2	J70536	ADP-ribosyl-nitrog
157	5	10.2	226	2	T23233	hypothetical prote	230	5	10.2	295	2	T34572	hypothetical prote
158	5	10.2	228	2	C75025	triose-phosphate i	231	5	10.2	296	2	T21070	hypothetical prote
159	5	10.2	228	2	S19932	glycine-rich prote	232	5	10.2	297	2	T18638	hypothetical prote
160	5	10.2	229	1	C45345	vif protein - capr	233	5	10.2	298	2	T33046	hypothetical prote
161	5	10.2	229	1	B43685	nonstructural prot	234	5	10.2	299	2	B55527	pqqG protein - Met
162	5	10.2	229	2	B40621	nisin biosynthesis	235	5	10.2	300	2	A43521	lymphocyte surface
163	5	10.2	229	2	B70158	conserved hypothet	236	5	10.2	300	2	G69476	hypothetical prote
164	5	10.2	230	2	A56210	neu differentiation	237	5	10.2	302	1	P3WMCC	3a protein - cowpe
165	5	10.2	231	2	G71201	triose-phosphate i	238	5	10.2	302	2	T36903	probable dihydrol
166	5	10.2	232	2	T09003	response regulator	239	5	10.2	302	2	S69725	hypothetical prote
167	5	10.2	232	2	D71442	hypothetical prote	240	5	10.2	302	2	T24187	hypothetical prote
168	5	10.2	233	2	C82360	cell division ATP-	241	5	10.2	304	2	G81417	cytochrome-c perox
169	5	10.2	233	2	S50154	hypothetical prote	242	5	10.2	304	2	T42521	probable UTP--gluc
170	5	10.2	235	1	A59036	cytochrome c554, t	243	5	10.2	304	2	T29184	hypothetical prote
171	5	10.2	236	1	A35649	cell surface prote	244	5	10.2	305	2	A69669	oligopeptide ABC t
172	5	10.2	236	1	A46472	cell surface prote	245	5	10.2	305	2	H82888	methionyl-tRNA for
173	5	10.2	238	1	A34378	endothelin 3 precu	246	5	10.2	307	2	T00687	hypothetical prote
174	5	10.2	238	1	S74682	spore germination	247	5	10.2	309	2	D71173	probable modificat
175	5	10.2	238	2	S33314	hypothetical prote	248	5	10.2	309	2	S57102	hypothetical prote

249	5	10.2	309	2	A70194	ABC transporter, A	322	5	10.2	370	2	S54297	protein phosphatas
250	5	10.2	309	2	T45719	hypothetical prote	323	5	10.2	370	2	G64654	hypothetical prote
251	5	10.2	310	2	JL0091	beta-lactamase (EC	324	5	10.2	371	1	AJMSQ3	glutamate--ammonia
252	5	10.2	310	2	S40808	polynucleotide ade	325	5	10.2	372	2	A42778	agglutinin precurs
253	5	10.2	310	2	B64882	conserved hypothet	326	5	10.2	373	1	AJMSQ	glutamate--ammonia
254	5	10.2	310	2	A69457	hypothetical prote	327	5	10.2	373	2	A70334	hypothetical prote
255	5	10.2	312	2	T47497	hypothetical prote	328	5	10.2	374	2	D72288	hypothetical prote
256	5	10.2	314	2	A71858	pyruvate ferredoxi	329	5	10.2	376	2	E31751	protein kinase cat
257	5	10.2	315	2	C83945	stage V sporulatio	330	5	10.2	378	2	S71201	biotin synthase (E
258	5	10.2	316	1	PBNSLC	beta-lactamase (EC	331	5	10.2	379	1	CBBO	ubiquinol--cytochr
259	5	10.2	318	2	T48507	probable GTP-bind	332	5	10.2	379	1	S17419	ubiquinol--cytochr
260	5	10.2	318	2	H71406	probable reverse t	333	5	10.2	379	1	S17405	ubiquinol--cytochr
261	5	10.2	319	2	S62810	adenine specific D	334	5	10.2	379	1	S43267	ubiquinol--cytochr
262	5	10.2	319	2	T21804	hypothetical prote	335	5	10.2	379	1	S43265	ubiquinol--cytochr
263	5	10.2	320	2	S09208	chorion protein s3	336	5	10.2	379	1	S17409	ubiquinol--cytochr
264	5	10.2	320	2	T25271	hypothetical prote	337	5	10.2	379	1	S43266	ubiquinol--cytochr
265	5	10.2	320	2	T37990	probable polysacch	338	5	10.2	379	1	S43268	ubiquinol--cytochr
266	5	10.2	322	2	T27966	hypothetical prote	339	5	10.2	379	1	S17414	ubiquinol--cytochr
267	5	10.2	322	2	T16633	hypothetical prote	340	5	10.2	379	1	S17407	ubiquinol--cytochr
268	5	10.2	323	2	S72915	hypothetical prote	341	5	10.2	379	1	S43269	ubiquinol--cytochr
269	5	10.2	324	2	S18547	alkanal monooxygen	342	5	10.2	379	1	S17413	ubiquinol--cytochr
270	5	10.2	324	2	A23866	transcription repr	343	5	10.2	379	1	S17418	ubiquinol--cytochr
271	5	10.2	325	2	A69595	probable modD prot	344	5	10.2	379	1	S17415	ubiquinol--cytochr
272	5	10.2	325	2	D70866	CCCH zinc finger p	345	5	10.2	379	1	S43263	ubiquinol--cytochr
273	5	10.2	325	2	S57977	hypothetical prote	346	5	10.2	379	1	S43262	ubiquinol--cytochr
274	5	10.2	325	2	T23208	Ig gamma-2 chain C	347	5	10.2	379	1	S17417	ubiquinol--cytochr
275	5	10.2	327	2	S06611	glucan endo-1,3-be	348	5	10.2	379	1	S43261	ubiquinol--cytochr
276	5	10.2	331	2	T02343	hypothetical prote	349	5	10.2	379	1	S41832	ubiquinol--cytochr
277	5	10.2	331	2	T18614	probable anion-upt	350	5	10.2	379	1	S43264	ubiquinol--cytochr
278	5	10.2	331	2	H81300	hypothetical prote	351	5	10.2	379	1	S43270	ubiquinol--cytochr
279	5	10.2	331	2	C64515	hypothetical prote	352	5	10.2	379	1	S17420	ubiquinol--cytochr
280	5	10.2	331	2	T13992	Sf16 protein, polli	353	5	10.2	379	1	S17406	ubiquinol--cytochr
281	5	10.2	332	2	A69224	polyferredoxin 4x2	354	5	10.2	379	2	E58851	ubiquinol--cytochr
282	5	10.2	332	2	H81876	probable membrane	355	5	10.2	379	2	S58057	ubiquinol--cytochr
283	5	10.2	332	2	B70965	probable integrase	356	5	10.2	379	2	S58085	ubiquinol--cytochr
284	5	10.2	333	2	S15238	O-antigen acetilas	357	5	10.2	379	2	S58448	ubiquinol--cytochr
285	5	10.2	334	2	H81406	probable integral	358	5	10.2	379	2	T11492	ubiquinol--cytochr
286	5	10.2	336	2	D69074	polyferredoxin 4x2	359	5	10.2	379	2	T10998	ubiquinol--cytochr
287	5	10.2	336	2	D70113	basic membrane pro	360	5	10.2	379	2	T11453	ubiquinol--cytochr
288	5	10.2	338	2	C64099	arDpGlucose 4,6-de	361	5	10.2	379	2	T11152	ubiquinol--cytochr
289	5	10.2	340	2	T28110	hypothetical prote	362	5	10.2	380	1	CBRT	ubiquinol--cytochr
290	5	10.2	341	2	S74759	hypothetical prote	363	5	10.2	380	1	S04840	ubiquinol--cytochr
291	5	10.2	342	2	T49687	lipoyltransferase	364	5	10.2	380	1	VCVGCN	coat protein - cuc
292	5	10.2	343	2	B38257	glucan endo-1,3-be	365	5	10.2	380	2	E58893	ubiquinol--cytochr
293	5	10.2	343	2	T50680	beta-1,3 glucanase	366	5	10.2	380	2	S70594	ubiquinol--cytochr
294	5	10.2	346	2	S55403	cymA protein precu	367	5	10.2	380	2	T11113	ubiquinol--cytochr
295	5	10.2	347	1	F64937	probable L-iditol	368	5	10.2	380	2	T11114	ubiquinol--cytochr
296	5	10.2	347	2	T07140	glucan endo-1,3-be	369	5	10.2	380	2	T11299	ubiquinol--cytochr
297	5	10.2	347	2	E83525	TolA protein PA097	370	5	10.2	380	2	S22415	membrane protein T
298	5	10.2	349	2	H82643	alcohol dehydrogen	371	5	10.2	380	2	T34568	hypothetical prote
299	5	10.2	349	2	S57453	polyferredoxin 4x2	372	5	10.2	380	2	T51053	hypothetical prote
300	5	10.2	350	2	JL0114	nitrogen regulatio	373	5	10.2	381	1	CBMS	ubiquinol--cytochr
301	5	10.2	350	2	T22450	hypothetical prote	374	5	10.2	381	2	S68140	ubiquinol--cytochr
302	5	10.2	351	2	T20270	hypothetical prote	375	5	10.2	381	2	D71943	hypothetical prote
303	5	10.2	352	2	F82284	S-adenosylmethioni	376	5	10.2	382	1	S33573	ubiquinol--cytochr
304	5	10.2	353	2	T34312	hypothetical prote	377	5	10.2	382	2	T11138	ubiquinol--cytochr
305	5	10.2	354	2	T04262	mitogen-activated	378	5	10.2	383	2	C75153	probable n2,n2-dim
306	5	10.2	355	2	T36273	hypothetical prote	379	5	10.2	385	1	CBBY	ubiquinol--cytochr
307	5	10.2	356	2	T03249	glucan endo-1,3-be	380	5	10.2	385	1	S15157	ubiquinol--cytochr
308	5	10.2	358	2	B81452	phosphoserine tran	381	5	10.2	385	2	S78660	ubiquinol--cytochr
309	5	10.2	358	2	A70746	hypothetical prote	382	5	10.2	386	2	T11832	ubiquinol--cytochr
310	5	10.2	359	2	D70155	fructose-bisphosph	383	5	10.2	389	2	T27085	hypothetical prote
311	5	10.2	359	2	G02221	CAGRI protein - hu	384	5	10.2	389	2	T23167	hypothetical prote
312	5	10.2	359	2	T22774	hypothetical prote	385	5	10.2	389	2	T47178	hypothetical prote
313	5	10.2	359	2	T19009	hypothetical prote	386	5	10.2	390	2	T51713	probable formamido
314	5	10.2	361	1	IBHUN	hydroxymethylbilan	387	5	10.2	392	2	T34095	zinc finger protei
315	5	10.2	361	1	IBRTE	hydroxymethylbilan	388	5	10.2	393	1	S22520	myb-related protei
316	5	10.2	361	1	IBMSGN	hydroxymethylbilan	389	5	10.2	394	2	T10200	hypothetical prote
317	5	10.2	362	2	B64527	M-protein - Helico	390	5	10.2	398	2	C82614	riboflavin biosynt
318	5	10.2	363	2	T26700	hypothetical prote	391	5	10.2	398	2	T46312	hypothetical prote
319	5	10.2	363	2	H71568	hypothetical prote	392	5	10.2	399	1	B49836	transcription fact
320	5	10.2	365	2	F64577	type I restriction	393	5	10.2	399	1	A43685	polymerase-associa
321	5	10.2	365	2	S72924	hypothetical prote	394	5	10.2	402	2	A40678	T-cell adhesio re

395 5 10.2 402 2 S46641 probable membrane
396 5 10.2 405 2 S46828 probable GTP-bind
397 5 10.2 407 2 E71665 bicyclomycin resis
398 5 10.2 408 2 T47498 hypothetical prote
399 5 10.2 409 2 G71935 type I restriction
400 5 10.2 410 2 T52294 patatin-like prote
401 5 10.2 411 2 S58094 hypothetical WW do
402 5 10.2 415 2 B69875 conserved hypotet
403 5 10.2 416 2 A41694 regulatory protein
404 5 10.2 416 2 T24564 hypothetical prote
405 5 10.2 419 2 B71481 probable clp prote
406 5 10.2 419 2 B46633 hypothetical prote
407 5 10.2 419 2 C71900 hypothetical prote
408 5 10.2 420 1 S34379 glycine hydroxymet
409 5 10.2 420 1 S22418 calsequestrin prec
410 5 10.2 421 1 D64100 glycine hydroxymet
411 5 10.2 422 2 H64489 hypothetical prote
412 5 10.2 422 2 S23237 glial growth facto
413 5 10.2 425 2 T46969 DEAD box RNA helic
414 5 10.2 425 2 T00720 hypothetical prote
415 5 10.2 426 2 T34108 hypothetical prote
416 5 10.2 426 2 T51373 hypothetical prote
417 5 10.2 427 2 JN0785 Carbon catabolite
418 5 10.2 428 2 S56629 mitosis-specific c
419 5 10.2 429 2 A83463 flagellar biosynth
420 5 10.2 430 2 T25489 hypothetical prote
421 5 10.2 431 2 G70344 probable glucose-6
422 5 10.2 431 2 T37621 hypothetical prote
423 5 10.2 433 2 S51773 transcription fact
424 5 10.2 436 2 B48937 cysteine aminopept
425 5 10.2 437 2 B46361 p element homolog
426 5 10.2 437 2 J50237 hypothetical 48K p
427 5 10.2 438 1 HVRK62 Ig mu chain C regi
428 5 10.2 443 2 T30619 probable serine/th
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432 5 10.2 451 1 ACBOG2 gamma-aminobutyric
433 5 10.2 451 2 JH0370 gamma-aminobutyric
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435 5 10.2 451 2 A81581 ABC transporter, p
436 5 10.2 452 2 T00113 undecaprenyl-phos
437 5 10.2 453 2 T30985 hypothetical prote
438 5 10.2 454 2 T20829 probable serine ca
439 5 10.2 455 2 S56695 1-aminocyclopropan
440 5 10.2 455 2 F72326 hemolysin-related
441 5 10.2 455 2 JC1224 nucleobindin precu
442 5 10.2 456 2 S20597 ribonuclease inhib
443 5 10.2 457 2 S55091 probable membrane
444 5 10.2 458 2 T10096 nifN protein - Met
445 5 10.2 460 2 T33420 hypothetical prote
446 5 10.2 461 2 S34472 MFH-1 protein - mo
447 5 10.2 461 2 H71717 3-deoxy-d-manno-oc
448 5 10.2 462 2 T38404 neu differentiation
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454 5 10.2 468 1 CYDKD2 delta-2-crystallin
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456 5 10.2 472 1 A49836 transcription fact
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459 5 10.2 476 2 JC5042 G protein-coupled
460 5 10.2 478 2 T11318 NADH dehydrogenase
461 5 10.2 481 1 S57294 carboxypeptidase D
462 5 10.2 482 2 G71603 chromatin-binding
463 5 10.2 482 2 S56945 protein YJL162c -
464 5 10.2 484 2 D64214 hypothetical prote
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466 5 10.2 486 2 T20482 hypothetical prote
467 5 10.2 487 2 JC2495 histamine H1 recep

468 5 10.2 488 2 A83367 probable phosphoma
469 5 10.2 488 2 E70234 conserved hypotet
470 5 10.2 491 2 A41632 histamine H1 recep
471 5 10.2 494 2 J50353 uridine diphosphog
472 5 10.2 498 2 A48205 interleukin-14 pre
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475 5 10.2 503 2 T13006 betaine aldehyde d
476 5 10.2 503 2 A54868 nuclear respirator
477 5 10.2 504 2 F64143 probable GTPase/GT
478 5 10.2 506 2 T40935 probable utp-gluc
479 5 10.2 506 2 A82876 oligopeptide trans
480 5 10.2 507 2 S73199 proteochlorophyllid
481 5 10.2 508 2 E64089 probable transport
482 5 10.2 508 2 S59870 fork head domain p
483 5 10.2 508 2 A31637 transcription fact
484 5 10.2 509 1 S14629 aldehyde dehydroge
485 5 10.2 509 2 S76731 hypothetical prote
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487 5 10.2 513 2 T02002 hypothetical prote
488 5 10.2 518 2 T39311 probable pre-mrna
489 5 10.2 519 2 T16712 hypothetical prote
490 5 10.2 526 2 T51372 hypothetical prote
491 5 10.2 527 2 T49241 pectinesterase-lik
492 5 10.2 529 2 A56516 nuclear localizati
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504 5 10.2 556 2 D69676 hypothetical prote
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509 5 10.2 567 2 T01032 hypothetical prote
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513 5 10.2 576 2 T43363 potassium channel
514 5 10.2 577 2 T07375 glucose-6-phosphat
515 5 10.2 582 2 T40198 transposase - Bact
516 5 10.2 585 2 T37526 probable transcrip
517 5 10.2 586 1 AJPMN1 asparagine synthas
518 5 10.2 586 2 S69182 asparagine synthas
519 5 10.2 586 2 S66697 probable membrane
520 5 10.2 588 2 T33815 hypothetical prote
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523 5 10.2 593 2 F64523 hypothetical prote
524 5 10.2 593 2 T24379 hypothetical prote
525 5 10.2 601 2 T42251 polypeptide N-acet
526 5 10.2 603 1 E64054 probable 5'-nucleo
527 5 10.2 603 2 T33134 hypothetical prote
528 5 10.2 604 2 T45627 replication factor
529 5 10.2 605 2 S67815 protein-tyrosine k
530 5 10.2 609 1 A48070 heat shock transcr
531 5 10.2 610 1 A49082 calcium-dependent
532 5 10.2 612 2 E81287 probable sugar tra
533 5 10.2 612 2 T29761 hypothetical prote
534 5 10.2 622 2 S51972 SPG72 protein - ye
535 5 10.2 623 2 T39001 probable exonuclea
536 5 10.2 628 2 S44629 F22B7, 10 protein -
537 5 10.2 630 2 A70117 probable long-chain
538 5 10.2 630 2 T07966 probable ethylene
539 5 10.2 633 2 J01242 Viral replicase 2
540 5 10.2 635 2 F70874 probable membrane

541	5	10.2	635	2	T06537	ethylene receptor	614	5	10.2	767	2	C71909	iron (III) diclita
542	5	10.2	636	2	T61718	neu differentiation	615	5	10.2	771	2	A84094	virulence-associat
543	5	10.2	636	2	T03439	probable ethylene-	616	5	10.2	771	2	T50299	hypothetical serin
544	5	10.2	637	2	C43273	herregulin precurs	617	5	10.2	773	2	I46059	beta-1 integrin su
545	5	10.2	639	2	I61719	neu differentiation	618	5	10.2	778	2	A64656	hypothetical prote
546	5	10.2	640	2	A43273	herregulin precurs	619	5	10.2	784	2	T13579	hypothetical prote
547	5	10.2	640	2	T72351	hypothetical prote	620	5	10.2	786	2	G41700	C5 protein - rabbi
548	5	10.2	644	2	S50429	dnak-type molecula	621	5	10.2	788	2	S44831	F54H12.1 protein -
549	5	10.2	645	2	T12159	NADH dehydrogenase	622	5	10.2	793	1	S60735	splicing factor SF
550	5	10.2	645	2	B43273	herregulin, splice	623	5	10.2	795	2	B83755	hypothetical prote
551	5	10.2	645	2	T51381	hypothetical prote	624	5	10.2	798	2	A28193	integrin beta-1 ch
552	5	10.2	645	2	T21829	hypothetical prote	625	5	10.2	798	2	B28193	integrin beta-1* c
553	5	10.2	648	2	S51409	hypothetical prote	626	5	10.2	798	2	B27079	fibronectin recept
554	5	10.2	654	2	E64245	periplasmic phosph	627	5	10.2	798	2	S01659	integrin beta-1 ch
555	5	10.2	654	2	B75587	probable N-glycosi	628	5	10.2	798	2	T19864	hypothetical prote
556	5	10.2	660	2	T40781	26S proteinase sub	629	5	10.2	799	1	IJMSFB	fibronectin recept
557	5	10.2	661	2	T24584	hypothetical prote	630	5	10.2	799	2	JC4126	integrin beta olig
558	5	10.2	662	2	I61722	neu differentiation	631	5	10.2	802	2	S25957	gene cox1 intron 2
559	5	10.2	662	2	H82401	conserved hypothet	632	5	10.2	803	1	IJCH3	integrin, band 3 p
560	5	10.2	667	2	S56829	probable membrane	633	5	10.2	803	2	S45916	hypothetical prote
561	5	10.2	667	2	T09482	ring finger protei	634	5	10.2	803	2	T40036	hypothetical prote
562	5	10.2	667	2	T09013	ring finger protei	635	5	10.2	805	2	T24431	hypothetical prote
563	5	10.2	670	2	T05222	hypothetical prote	636	5	10.2	807	2	B71605	hypothetical prote
564	5	10.2	674	2	S39476	kinase-like transm	637	5	10.2	813	2	G75331	ATP-dependent prot
565	5	10.2	680	2	A28121	major merozoite su	638	5	10.2	815	2	D83785	glycogen phosphory
566	5	10.2	682	1	H64485	replication licens	639	5	10.2	816	2	T21713	hypothetical prote
567	5	10.2	685	2	G69864	penicillin-binding	640	5	10.2	816	2	T48123	hypothetical prote
568	5	10.2	686	2	T03123	DNA packaging prot	641	5	10.2	817	2	A48721	titin, muscle - ch
569	5	10.2	686	2	T08919	hypothetical prote	642	5	10.2	817	2	S53921	hypothetical prote
570	5	10.2	687	2	T08877	Modin - Podospora	643	5	10.2	820	2	B83739	exonuclease ABC (
571	5	10.2	687	2	T39838	hypothetical prote	644	5	10.2	822	2	T01095	hypothetical prote
572	5	10.2	688	2	S39491	protochlorophyllid	645	5	10.2	824	2	T16028	hypothetical prote
573	5	10.2	689	1	S29621	UDPglucose 4-epime	646	5	10.2	834	1	QXB31	gene cox1 intron 1
574	5	10.2	689	2	F64698	conserved hypothet	647	5	10.2	834	2	S78642	gene cox1 intron 1
575	5	10.2	689	2	T18494	hypothetical prote	648	5	10.2	845	2	T40955	hypothetical prote
576	5	10.2	690	2	T27508	hypothetical prote	649	5	10.2	848	2	B84107	hypothetical prote
577	5	10.2	691	2	H71004	hypothetical prote	650	5	10.2	851	2	S12159	env protein - huma
578	5	10.2	691	2	T31552	hypothetical prote	651	5	10.2	856	2	B81399	probable periplasm
579	5	10.2	692	1	PABY12	phosphoprotein pho	652	5	10.2	865	1	I5ECTP	DNA topoisomerase
580	5	10.2	692	2	F71821	hypothetical prote	653	5	10.2	867	2	T02579	hypothetical prote
581	5	10.2	692	2	T05111	hypothetical prote	654	5	10.2	874	2	T00491	capsid protein pre
582	5	10.2	696	2	T12160	NADH dehydrogenase	655	5	10.2	875	2	T30023	hypothetical prote
583	5	10.2	702	2	T13058	NADH dehydrogenase	656	5	10.2	880	1	SYBSVS	valine--tRNA ligas
584	5	10.2	702	2	S41685	NGG1 protein - yea	657	5	10.2	884	2	S61569	hypothetical prote
585	5	10.2	704	2	I39805	cyclomaltodextrin	658	5	10.2	884	2	T20405	hypothetical prote
586	5	10.2	706	2	T20052	hypothetical prote	659	5	10.2	886	2	A48586	suppressor of hair
587	5	10.2	707	2	A46302	PTB-associated spl	660	5	10.2	887	2	S57219	phosphatidylinosit
588	5	10.2	709	2	T39930	probable atp-depen	661	5	10.2	896	2	I56563	interleukin-3 rece
589	5	10.2	710	2	S63598	cyclomaltodextrin	662	5	10.2	899	2	B48586	suppressor of hair
590	5	10.2	710	2	T21339	hypothetical prote	663	5	10.2	902	2	T47966	hypothetical prote
591	5	10.2	710	2	G82689	soluble lytic mure	664	5	10.2	908	2	S07649	gene coI intron 1
592	5	10.2	711	2	T12525	hypothetical prote	665	5	10.2	915	2	T21773	hypothetical prote
593	5	10.2	711	2	D83897	catalase katB [imp	666	5	10.2	918	2	A44257	interleukin-6 sign
594	5	10.2	713	2	JE0230	NADPH-cytochrome P	667	5	10.2	919	2	S37786	hypothetical prote
595	5	10.2	714	2	T35770	hypothetical prote	668	5	10.2	923	2	T41350	meiotic recombina
596	5	10.2	715	2	S08450	hypothetical prote	669	5	10.2	926	2	T38198	COPII coated vesic
597	5	10.2	718	1	ALBSMX	cyclomaltodextrin	670	5	10.2	927	2	T21772	hypothetical prote
598	5	10.2	718	1	ALBSG6	cyclomaltodextrin	671	5	10.2	929	2	T52517	hypothetical prote
599	5	10.2	718	1	ALBSGC	cyclomaltodextrin	672	5	10.2	930	2	T15977	hypothetical prote
600	5	10.2	722	2	B71728	probable peptidase	673	5	10.2	934	2	T15567	hypothetical prote
601	5	10.2	723	2	T02477	hypothetical prote	674	5	10.2	935	2	T29390	hypothetical prote
602	5	10.2	727	2	A71069	hypothetical prote	675	5	10.2	940	2	A40985	projectin - fruit
603	5	10.2	729	2	T23972	hypothetical prote	676	5	10.2	940	2	T00056	hypothetical prote
604	5	10.2	736	2	S69074	hypothetical prote	677	5	10.2	944	2	T28734	hypothetical prote
605	5	10.2	736	2	T06271	probable ethylene-	678	5	10.2	944	2	S01909	hairy wing suppl
606	5	10.2	737	2	G82262	probable exopolysa	679	5	10.2	945	2	B82001	valyl-tRNA synthet
607	5	10.2	740	2	T51619	probable ethylene	680	5	10.2	945	2	F81230	valyl-tRNA synthet
608	5	10.2	741	2	T16992	ethylene receptor	681	5	10.2	948	2	T26417	hypothetical prote
609	5	10.2	751	1	T29357	1-phosphatidylinos	682	5	10.2	950	2	A71655	hypothetical prote
610	5	10.2	754	2	S711783	ETR1 protein homol	683	5	10.2	952	2	T18837	hypothetical prote
611	5	10.2	754	2	T52288	ethylene receptor	684	5	10.2	958	2	T04870	cellulose synthase
612	5	10.2	755	2	T20320	hypothetical prote	685	5	10.2	959	2	S48962	MSH1 protein - yea
613	5	10.2	755	2	S42462	structural polypro	686	5	10.2	959	2	T23094	hypothetical prote

687	5	10.2	961	2	T23095	hypothetical prote	760	10.2	1328	1	S04273	retrovirus-related
688	5	10.2	970	2	S63059	hypothetical prote	761	10.2	1330	2	A36373	hypothetical prote
689	5	10.2	973	2	T41201	isoleucyl-tRNA syn	762	10.2	1353	2	T00347	hypothetical prote
690	5	10.2	975	2	T48107	hypothetical prote	763	10.2	1358	2	S33653	probable serine/th
691	5	10.2	976	2	S45738	pleiotropic drug r	764	10.2	1367	2	S51959	hypothetical prote
692	5	10.2	992	2	S43396	protein L precursor	765	10.2	1367	2	T18466	hypothetical prote
693	5	10.2	996	2	S70646	transcription fact	766	10.2	1380	2	S57150	ZMS1 protein - yea
694	5	10.2	1001	2	S74544	translation initia	767	10.2	1385	2	T25828	hypothetical prote
695	5	10.2	1002	2	S62035	isoleucine--tRNA l	768	10.2	1390	2	T30346	insulin receptor -
696	5	10.2	1003	2	C71139	hypothetical prote	769	10.2	1405	2	T40607	probable dna-direc
697	5	10.2	1007	2	T24643	hypothetical prote	770	10.2	1419	1	DVZQF	multidrug resistan
698	5	10.2	1008	2	T04462	hypothetical prote	771	10.2	1428	2	T13926	probable protein p
699	5	10.2	1021	2	G75403	DNA topoisomerase	772	10.2	1429	2	T19422	hypothetical prote
700	5	10.2	1036	2	T38734	hypothetical prote	773	10.2	1440	2	JC6312	protein-tyrosine-p
701	5	10.2	1037	2	T13350	transcription fact	774	10.2	1468	2	S58250	DNA-directed DNA p
702	5	10.2	1039	2	T28905	hypothetical prote	775	10.2	1471	1	S30790	myosin MYO4 - yea
703	5	10.2	1051	2	T43233	carbamoyl-phosphat	776	10.2	1477	2	T18534	protein-tyrosine k
704	5	10.2	1052	2	C84221	hypothetical 114K	777	10.2	1479	2	T17401	transcription regu
705	5	10.2	1059	2	G83706	lanthibiotic mersac	778	10.2	1482	2	T34010	hypothetical prote
706	5	10.2	1062	2	S09834	hypothetical prote	779	10.2	1492	2	T18560	DNA-directed DNA p
707	5	10.2	1076	1	A35622	nuclear pore prote	780	10.2	1513	2	T31434	densin-180 - rat
708	5	10.2	1083	2	T23031	hypothetical prote	781	10.2	1513	2	T28158	probable DNA-direc
709	5	10.2	1084	2	S23319	hypothetical prote	782	10.2	1525	1	GNWVS	genome polyprotein
710	5	10.2	1086	2	S54876	NAD(P)+ transhydro	783	10.2	1539	2	T48059	ABC transporter-li
711	5	10.2	1086	2	S74251	phosphorylase kina	784	10.2	1570	2	T18272	1-phosphatidylinos
712	5	10.2	1093	2	S74250	phosphorylase kina	785	10.2	1603	1	VJWK5	vitellogenin vit-5
713	5	10.2	1098	1	YGBSG1	phenylalanine race	786	10.2	1650	2	T27864	hypothetical prote
714	5	10.2	1104	1	A36866	microbial collagen	787	10.2	1672	2	T46237	hypothetical prote
715	5	10.2	1106	2	T18739	hypothetical prote	788	10.2	1683	2	T30885	complement compone
716	5	10.2	1106	2	T31742	hypothetical prote	789	10.2	1700	2	S08167	Balbani ring 3 pr
717	5	10.2	1107	2	T20578	hypothetical prote	790	10.2	1712	2	C71618	hypothetical prote
718	5	10.2	1113	2	H84105	hypothetical prote	791	10.2	1717	2	T50247	probable helicase
719	5	10.2	1119	2	T20577	hypothetical prote	792	10.2	1752	2	T48965	hypothetical prote
720	5	10.2	1122	2	T47424	hypothetical prote	793	10.2	1772	2	A45532	major merozoite su
721	5	10.2	1127	2	T25804	hypothetical prote	794	10.2	1872	2	T00339	hypothetical prote
722	5	10.2	1131	2	T19442	hypothetical prote	795	10.2	1873	2	A30063	dihydropyridine re
723	5	10.2	1134	2	T20332	hypothetical prote	796	10.2	1906	1	S68235	myosin-light-chain
724	5	10.2	1140	2	T20984	hypothetical prote	797	10.2	1974	2	T30010	hypothetical prote
725	5	10.2	1144	1	A43271	nitric-oxide synth	798	10.2	2077	2	T43991	large tegument pro
726	5	10.2	1144	2	A36968	PI-like adhesin pr	799	10.2	2077	2	T44178	large tegument pro
727	5	10.2	1147	1	S47647	nitric-oxide synth	800	10.2	2136	2	A05037	hypothetical prote
728	5	10.2	1147	1	S56575	nitric-oxide synth	801	10.2	2144	2	S71490	ash1 protein - fru
729	5	10.2	1147	1	S38253	nitric-oxide synth	802	10.2	2206	1	GNNY21	genome polyprotein
730	5	10.2	1147	1	I53165	nitric-oxide synth	803	10.2	2207	1	GNNY1P	genome polyprotein
731	5	10.2	1147	2	JC5027	nitric-oxide synth	804	10.2	2209	1	GNNY2P	genome polyprotein
732	5	10.2	1147	2	JC5028	nitric-oxide synth	805	10.2	2209	1	GNNY3P	genome polyprotein
733	5	10.2	1147	2	JC5029	nitric-oxide synth	806	10.2	2214	1	A48548	genome polyprotein
734	5	10.2	1147	2	S65440	nitric-oxide synth	807	10.2	2298	2	T49648	hypothetical prote
735	5	10.2	1151	2	T18535	high molecular mas	808	10.2	2301	1	GNNYTN	genome polyprotein
736	5	10.2	1154	2	S43275	hypothetical prote	809	10.2	2303	1	GNNYTM	genome polyprotein
737	5	10.2	1169	2	C71639	hypothetical prote	810	10.2	2303	1	GNNYTP	genome polyprotein
738	5	10.2	1187	1	JC4155	protein-tyrosine-p	811	10.2	2303	2	SI3554	genome polyprotein
739	5	10.2	1189	1	JC2366	protein-tyrosine-p	812	10.2	2342	2	T18200	fatty-acid synthas
740	5	10.2	1196	1	DNBEV1	major DNA-binding	813	10.2	2437	2	S53611	MIBP1 protein - ra
741	5	10.2	1196	1	DNBEKS	DNA-binding protei	814	10.2	2500	1	WMHUE2	HIV-EP2 enhancer-b
742	5	10.2	1196	1	DNBEHF	DNA-binding protei	815	10.2	2555	2	C69681	peptide synthetase
743	5	10.2	1197	1	A48350	DNA-binding protei	816	10.2	2610	2	T20968	hypothetical prote
744	5	10.2	1199	2	T18348	probable pol poly	817	10.2	2630	2	T08868	polyprotein pl - A
745	5	10.2	1214	2	JC7259	Smad interacting p	818	10.2	2647	2	T28161	hypothetical prote
746	5	10.2	1219	2	S54570	probable membrane	819	10.2	2657	2	T18497	hypothetical prote
747	5	10.2	1221	2	T30529	ubiquitin carboxyl	820	10.2	2962	2	T19756	hypothetical prote
748	5	10.2	1230	2	T18256	probable serine/th	821	10.2	3122	2	T17202	DNA-directed DNA p
749	5	10.2	1230	2	T18259	serine/threonine p	822	10.2	3176	1	CGHU3A	collagen alpha 3(V
750	5	10.2	1240	2	T04833	hypothetical prote	823	10.2	3655	2	T38084	TRAP-like protein
751	5	10.2	1253	1	VHWV	structural polypro	824	10.2	3759	2	A35085	thiorax protein
752	5	10.2	1272	2	S60999	ubiquitin-specific	825	10.2	3871	2	T22812	hypothetical prote
753	5	10.2	1279	2	E64709	type IIS restricti	826	10.2	4377	2	A55575	ankyrin 3, long sp
754	5	10.2	1281	2	JC5368	dynactin 1 - mouse	827	10.2	4660	2	T42737	gp330 protein prec
755	5	10.2	1291	1	S05465	retrovirus-related	828	10.2	4910	2	S64942	probable membrane
756	5	10.2	1306	2	T28313	ORF M5V152 probabl	829	10.2	6658	2	T13931	projectin - fruit
757	5	10.2	1306	2	A60165	sodium channel pro	830	10.2	6805	2	S20901	titin - rabbit (fr
758	5	10.2	1321	2	S52863	DNA-binding protei	831	10.2	6839	2	S57242	twitchin [similar
759	5	10.2	1325	2	S16129	dynein-associated	832	10.2	7160	2	T27935	hypothetical prote

833	5	10.2	26926	1	I38344	titin, cardiac mus	906	4	8.2	39	2	S43283	gallinacin - chick
834	4	8.2	7	2	A61081	tryptophyllin, bas	907	4	8.2	39	2	H82657	hypothetical prote
835	4	8.2	12	2	S71380	lebetin 1 isoform	908	4	8.2	40	2	A82382	hypothetical prote
836	4	8.2	19	1	LFSAp9	emC leader peptid	909	4	8.2	40	2	S71301	ICL5 protein - Par
837	4	8.2	22	2	PC4388	sulfite reductase	910	4	8.2	41	2	I49419	insulin II precurs
838	4	8.2	24	2	S40666	hypothetical prote	911	4	8.2	41	2	S38918	hypothetical prote
839	4	8.2	25	2	A45920	cellulase (EC 3.2.	912	4	8.2	41	2	G72312	hypothetical prote
840	4	8.2	25	2	PC4389	sulfite reductase	913	4	8.2	41	2	H82380	hypothetical prote
841	4	8.2	26	2	S61590	beta-lactoglobulin	914	4	8.2	42	2	S06812	myosin heavy chain
842	4	8.2	26	2	S65604	sec c 1 protein -	915	4	8.2	42	2	S06813	myosin heavy chain
843	4	8.2	27	2	E44829	homeotic protein H	916	4	8.2	42	2	A05049	hypothetical prote
844	4	8.2	27	2	A58997	kappa-conotoxin PV	917	4	8.2	42	2	T01609	hypothetical prote
845	4	8.2	28	2	S47614	zinc finger protei	918	4	8.2	42	2	T02556	hypothetical prote
846	4	8.2	29	2	E64586	hypothetical prote	919	4	8.2	43	2	PH0883	ig kappa chain V r
847	4	8.2	30	2	I68109	interferon alpha-W	920	4	8.2	43	2	T06853	photosystem II pr
848	4	8.2	32	2	E82089	hypothetical prote	921	4	8.2	43	2	E82107	hypothetical prote
849	4	8.2	33	2	PQ0416	RNA-directed RNA p	922	4	8.2	44	2	S35146	photosystem II pro
850	4	8.2	33	2	PQ0410	RNA-directed RNA p	923	4	8.2	44	2	S34838	tyrosine-rich acid
851	4	8.2	33	2	A82288	hypothetical prote	924	4	8.2	44	2	S21028	m-factor precursor
852	4	8.2	34	2	PH1748	ig heavy chain V r	925	4	8.2	45	1	C64901	ribosomal protein
853	4	8.2	35	2	I49403	complement factor	926	4	8.2	45	2	F71470	probable L36 ribos
854	4	8.2	35	2	D82125	hypothetical prote	927	4	8.2	45	2	B72017	L36 ribosomal prot
855	4	8.2	36	1	NYPGY	neuropeptide Y - p	928	4	8.2	45	2	A69296	hypothetical prote
856	4	8.2	36	2	S07052	neuropeptide Y - s	929	4	8.2	46	2	I39904	GIP cyclohydrolase
857	4	8.2	36	2	A30485	neuropeptide Y - s	930	4	8.2	46	2	I48944	cellular disintegr
858	4	8.2	36	2	B30485	neuropeptide Y - g	931	4	8.2	47	2	A35982	echistatin alpha-2
859	4	8.2	36	2	A48540	neuropeptide Y - c	932	4	8.2	47	2	E70193	hypothetical prote
860	4	8.2	36	2	A39393	neuropeptide Y - l	933	4	8.2	47	2	I40320	vir-repressed prot
861	4	8.2	36	2	B81820	hypothetical prote	934	4	8.2	48	2	S26133	outer membrane pro
862	4	8.2	36	2	S70092	hypothetical prote	935	4	8.2	48	2	S26117	outer membrane pro
863	4	8.2	36	2	B82734	hypothetical prote	936	4	8.2	48	2	F82015	hypothetical prote
864	4	8.2	37	1	R5R236	ribosomal protein	937	4	8.2	49	2	S30503	protein kinase Mpk
865	4	8.2	37	1	R5NT36	ribosomal protein	938	4	8.2	49	2	A32029	echistatin alpha-1
866	4	8.2	37	1	R5LV36	ribosomal protein	939	4	8.2	49	2	S03222	hypothetical prote
867	4	8.2	37	1	R5PWR1	ribosomal protein	940	4	8.2	49	2	B64812	hypothetical prote
868	4	8.2	37	1	R5EG36	ribosomal protein	941	4	8.2	49	2	A54547	ribosomal protein
869	4	8.2	37	1	R5BS36	ribosomal protein	942	4	8.2	50	2	S53431	echistatin beta -
870	4	8.2	37	1	R5IT36	ribosomal protein	943	4	8.2	50	2	D72072	hypothetical prote
871	4	8.2	37	2	JH0709	calcitonin gene-re	944	4	8.2	51	1	INWHP	insulin - sperm wh
872	4	8.2	37	2	B60963	charybdotoxin 2 -	945	4	8.2	51	1	INWHF	insulin - finback
873	4	8.2	37	2	T07351	ribosomal protein	946	4	8.2	51	1	INHY	insulin - hamster
874	4	8.2	37	2	A71833	ribosomal protein	947	4	8.2	51	1	INMSP	insulin - Egyptian
875	4	8.2	37	2	G71351	probable ribosomal	948	4	8.2	51	1	INMKSQ	insulin - common s
876	4	8.2	37	2	S78391	ribosomal protein	949	4	8.2	51	1	A61125	insulin - American
877	4	8.2	37	2	A64682	ribosomal protein	950	4	8.2	51	2	JQ0362	insulin - North Am
878	4	8.2	37	2	B49923	ribosomal protein	951	4	8.2	51	2	S26101	outer membrane pro
879	4	8.2	37	2	C64219	ribosomal protein	952	4	8.2	51	2	T07344	hypothetical prote
880	4	8.2	37	2	S58585	ribosomal protein	953	4	8.2	51	2	H81605	hypothetical prote
881	4	8.2	37	2	S62820	ribosomal protein	954	4	8.2	51	2	B82676	hypothetical prote
882	4	8.2	37	2	S73217	ribosomal protein	955	4	8.2	52	1	RUME	rubredoxin - Megas
883	4	8.2	37	2	S78257	ribosomal protein	956	4	8.2	52	2	A60655	hypothetical prote
884	4	8.2	37	2	B70566	probable ribosomal	957	4	8.2	52	2	PH0881	ig kappa chain V r
885	4	8.2	37	2	T06947	ribosomal protein	958	4	8.2	53	2	B81835	hypothetical prote
886	4	8.2	37	2	T07519	ribosomal protein	959	4	8.2	53	2	J50105	hypothetical 5.8k
887	4	8.2	37	2	A82057	ribosomal protein	960	4	8.2	53	2	T33567	hypothetical prote
888	4	8.2	37	2	G82917	ribosomal protein	961	4	8.2	53	2	D83937	spore coat protein
889	4	8.2	37	2	A82003	50S ribosomal prot	962	4	8.2	54	2	I37018	T-cell phorbol-12-
890	4	8.2	37	2	E81254	50S ribosomal prot	963	4	8.2	54	2	PWXL8	H+-transporting AT
891	4	8.2	37	2	F75312	ribosomal protein	964	4	8.2	55	1	T11538	H+-transporting AT
892	4	8.2	37	2	T35555	ribosomal protein	965	4	8.2	55	2	T11197	H+-transporting AT
893	4	8.2	37	2	PN0550	metabotropic gluta	966	4	8.2	55	2	S77794	hypothetical prote
894	4	8.2	38	1	R5EC36	ribosomal protein	967	4	8.2	55	2	S30332	proteinase inhibit
895	4	8.2	38	2	S17989	ribosomal protein	968	4	8.2	56	2	I38268	protein-tyrosine k
896	4	8.2	38	2	S77481	ribosomal protein	969	4	8.2	56	2	I51029	calcitonin 1 - pin
897	4	8.2	38	2	H83113	50S ribosomal prot	970	4	8.2	56	2	T10959	proline-rich prote
898	4	8.2	38	2	A29790	trichosanthin (ver	971	4	8.2	56	2	I40042	truncated endonuc
899	4	8.2	38	2	A70239	hypothetical prote	972	4	8.2	56	2	T27437	hypothetical prote
900	4	8.2	38	2	I70014	kallikrein - mouse	973	4	8.2	57	1	R5EC32	ribosomal protein
901	4	8.2	38	2	I70032	kallikrein - mouse	974	4	8.2	57	2	PH0879	ig kappa chain V r
902	4	8.2	38	2	S71381	lebetin 2 isoform	975	4	8.2	57	2	T07127	RNA-directed DNA p
903	4	8.2	39	2	I49418	insulin I precursor	976	4	8.2	57	2	F59098	hypothetical prote
904	4	8.2	39	2	B70162	ribosomal protein	977	4	8.2	57	2	E82733	hypothetical prote
905	4	8.2	39	2	S43282	gallinacin - chick	978	4	8.2	58	2	S71422	argininosuccinate

979 4 8.2 58 2 S58628 hypothetical prote
980 4 8.2 58 2 C83918 hypothetical prote
981 4 8.2 58 2 H82736 hypothetical prote
982 4 8.2 59 2 T12647 NADH dehydrogenase
983 4 8.2 59 2 I51260 calctonin I - pin
984 4 8.2 59 2 T07432 photosystem II pro
985 4 8.2 59 2 J00811 hypothetical 6.8K
986 4 8.2 59 2 H82107 hypothetical prote
987 4 8.2 59 2 H69218 hypothetical prote
988 4 8.2 60 2 D69133 DNA-dependent RNA
989 4 8.2 60 2 F75618 hypothetical prote
990 4 8.2 61 1 T1E8H proteinase inhibit
991 4 8.2 61 2 A71868 hypothetical prote
992 4 8.2 61 2 F81844 hypothetical prote
993 4 8.2 61 2 A69524 hypothetical prote
994 4 8.2 61 2 J01086 nodulin-14 precurs
995 4 8.2 61 2 A45099 calcium channel al
996 4 8.2 62 2 S42265 Ig kappa chain V r
997 4 8.2 62 2 JN0733 hypothetical 7.5K
998 4 8.2 62 2 D71571 hypothetical prote
999 4 8.2 62 2 T19376 hypothetical prote
1000 4 8.2 62 2 D83979 hypothetical prote

ALIGNMENTS

RESULT 1
MGNZ
major surface glycoprotein G - human respiratory syncytial virus
C:Species: human respiratory syncytial virus
C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 24-Sep-1999
C:Accession: A94048; A93599; A04039
R:Wertz, G.W.; Collins, P.B.; Huang, Y.; Gruber, C.; Levine, S.; Ball, L.A.
Proc. Natl. Acad. Sci. U.S.A. 82, 4075-4079, 1985
A:Title: Nucleotide sequence of the G protein gene of human respiratory syncytial virus
A:Reference number: A94048; MUID:85216636
A:Accession: A94048
A:Molecule type: mRNA
A:Residues: 1-298 <WER>
A:Cross-references: GB:M11486; GB:K01459; GB:K02719; GB:K03348; GB:K03349; GB:M11217; GB:7.1; PID:g333932
A:Note: Residues 207-298 are identical with residues 376-467 of the nucleocapsid protein
A:Note: this protein may carry 40-80 separate O-linked carbohydrate chains distributed a
R:Satake, M.; Coligan, J.E.; Elango, N.; Norrby, E.; Venkatesan, S.
Nucleic Acids Res. 13, 7795-7812, 1985
A:Title: Respiratory syncytial virus envelope glycoprotein (G) has a novel structure.
A:Reference number: A93599; MUID:86067198
A:Accession: A93599
A:Molecule type: mRNA
A:Residues: 1-298 <SAT>
A:Cross-references: GB:X03149; MID:g60997; PIDN:CAA26928.1; PID:g60998
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:38-66/Domain: transmembrane #status predicted <TN>
F:85,135,237,251/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 49; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 3.9e-45;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNDFHFEVFNPCSGSNNPTCWAICKRIPNKKPGK 49
|||||
Db 149 KORQKPPSKPNDFHFEVFNPCSGSNNPTCWAICKRIPNKKPGK 197

RESULT 2
JQ1205
attachment protein - human respiratory syncytial virus (strain RSB1734)
N:Alternate names: G protein
C:Species: human respiratory syncytial virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997

C:Accession: JQ1205
R:Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
A:Title: Identification of variable domains of the attachment (G) protein of subgroup
A:Reference number: JQ1204; MUID:91374005
A:Accession: JQ1205
A:Molecule type: mRNA
A:Residues: 1-297 <CAN>
C:Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract
in children and adults.
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:85,103,135,237,251,273/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 98.0%; Score 48; DB 2; Length 297;
Best Local Similarity 100.0%; Pred. No. 4.5e-44;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNDFHFEVFNPCSGSNNPTCWAICKRIPNKKPGK 48
|||||
Db 149 KORQKPPSKPNDFHFEVFNPCSGSNNPTCWAICKRIPNKKPGK 196

RESULT 3
JQ1204
attachment protein - human respiratory syncytial virus (strain RSB642)
N:Alternate names: G protein
C:Species: human respiratory syncytial virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C:Accession: JQ1204
R:Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
A:Title: Identification of variable domains of the attachment (G) protein of subgroup
A:Reference number: JQ1204; MUID:91374005
A:Accession: JQ1204
A:Molecule type: mRNA
A:Residues: 1-297 <CAN>
C:Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract
in children and adults.
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:85,103,135,144,237,273/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 98.0%; Score 48; DB 2; Length 297;
Best Local Similarity 100.0%; Pred. No. 4.5e-44;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNDFHFEVFNPCSGSNNPTCWAICKRIPNKKPGK 48
|||||
Db 149 KORQKPPSKPNDFHFEVFNPCSGSNNPTCWAICKRIPNKKPGK 196

RESULT 4
JQ1208
attachment protein - human respiratory syncytial virus (strain RSB6256)
N:Alternate names: G protein
C:Species: human respiratory syncytial virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C:Accession: JQ1208
R:Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
A:Title: Identification of variable domains of the attachment (G) protein of subgroup
A:Reference number: JQ1204; MUID:91374005
A:Accession: JQ1208
A:Molecule type: mRNA
A:Residues: 1-297 <CAN>
C:Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract
in children and adults.
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:85,103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covalent) #status pred


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Query Match      81.6%; Score 40; DB 2; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.7e-35;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KPNDFHFEVFNVPSCSNNPTCWAICKRIPNKKPGKK 49
|||||
Db 158 KPNDFHFEVFNVPSCSNNPTCWAICKRIPNKKPGKK 197

RESULT 5
JC5680
protein - human respiratory syncytial virus (strain RSB5857)
C:Species: human respiratory syncytial virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C:Accession: JQ1206
R:Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
A:Title: Identification of variable domains of the attachment (G) protein of subgroup A
A:Reference number: JQ1204; MUID:91374005
A:Accession: JQ1206
A:Molecule type: mRNA
A:Residues: 1-297 <CAN>
A:Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract in
children and adults.
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:85,103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match      81.6%; Score 40; DB 2; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.7e-35;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KPNDFHFEVFNVPSCSNNPTCWAICKRIPNKKPGKK 49
|||||
Db 158 KPNDFHFEVFNVPSCSNNPTCWAICKRIPNKKPGKK 197

RESULT 6
MGNZRL
major surface glycoprotein G - human respiratory syncytial virus (strain Long)
C:Species: human respiratory syncytial virus
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
C:Accession: A32703; S12279
R:Johnson, P.R.; Spriggs, M.K.; Olmsted, R.A.; Collins, P.L.
Proc. Natl. Acad. Sci. U.S.A. 84, 5625-5629, 1987
A:Title: The G glycoprotein of human respiratory syncytial viruses of subgroups A and B
A:Reference number: A32703; MUID:87289657
A:Accession: A32703
A:Molecule type: mRNA
A:Residues: 1-298 <JOH>
A:Cross-references: GB:M17212; NID:g3333940; PIDN:AAA47411.1; PID:g333941
R:Garcia-Barreno, B.; Portela, A.; Delgado, T.; Lopez, J.A.; Melero, J.A.
EMBO J. 9, 4181-4187, 1990
A:Title: Frame shift mutations as a novel mechanism for the generation of neutralization
A:Reference number: S12279; MUID:91065351
A:Accession: S12279
A:Molecule type: mRNA
A:Residues: 1-298 <GAR>
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:41-63/Domain: transmembrane #status predicted <TMN>
F:85,103,135,179,237,250,251,273,294/Binding site: carbohydrate (Asn) (covalent) #status

Query Match      81.6%; Score 40; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.7e-35;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KPNDFHFEVFNVPSCSNNPTCWAICKRIPNKKPGKK 49
|||||
Db 158 KPNDFHFEVFNVPSCSNNPTCWAICKRIPNKKPGKK 197

RESULT 7
JC5680
protein - Human respiratory syncytial virus
C:Species: Human respiratory syncytial virus
C:Date: 11-Nov-1997 #sequence_revision 11-Nov-1997 #text_change 26-Feb-1998
C:Accession: JC5680
R:Geng, X.; Wang, Z.; Qian, Y.; Zhu, R.; Deng, J.; Du, J.; Zhu, Z.
Chinese J. Virol. 12, 317-322, 1996
A:Title: Molecular analysis of G protein gene of a respiratory syncytial virus strain
A:Reference number: JC5680
A:Accession: JC5680
A:Molecule type: mRNA
A:Residues: 1-298 <GEN>
A:Experimental source: strain B79
A:Note: the authors translated the codon TTT for residue 165 and 170 as Glu, TTC for
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
F:1-38/Domain: intracellular #status predicted <INT>
F:39-66/Domain: transmembrane #status predicted <TMN>
F:67-298/Domain: extracellular #status predicted <EXC>

Query Match      81.6%; Score 40; DB 2; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.7e-35;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KPNDFHFEVFNVPSCSNNPTCWAICKRIPNKKPGKK 49
|||||
Db 158 KPNDFHFEVFNVPSCSNNPTCWAICKRIPNKKPGKK 197

RESULT 8
JQ1209
attachment protein - human respiratory syncytial virus (strain RSB6614)
N:Alternate names: G protein
C:Species: human respiratory syncytial virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C:Accession: JQ1209
R:Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
A:Title: Identification of variable domains of the attachment (G) protein of subgroup
A:Reference number: JQ1204; MUID:91374005
A:Accession: JQ1209
A:Molecule type: mRNA
A:Residues: 1-297 <CAN>
A:Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract
er children and adults.
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:85,103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covalent) #status pred

Query Match      71.4%; Score 35; DB 2; Length 297;
Best Local Similarity 100.0%; Pred. No. 3.8e-30;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 FHFEVFNVPSCSNNPTCWAICKRIPNKKPGKK 49
|||||
Db 163 FHFEVFNVPSCSNNPTCWAICKRIPNKKPGKK 197

RESULT 9
JQ1207
attachment protein - human respiratory syncytial virus (strain RSB6190)
N:Alternate names: G protein
C:Species: human respiratory syncytial virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C:Accession: JQ1207
R:Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
```

A>Title: Identification of variable domains of the attachment (G) protein of subgroup A
A:Reference number: JQ1204; MUID:91374005
A:Molecule type: mRNA
A:Residues: 1-298 <CAN>
A>Note: The authors translated the codon ACC for residue 4 as Asn and AGC for residue 22 as Ser. The authors also noted that the codon ACC for residue 4 as Asn and AGC for residue 22 as Ser. The authors also noted that the codon ACC for residue 4 as Asn and AGC for residue 22 as Ser.
C:Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract illness in children and adults.
C:Superfamily: respiratory syncytial virus-major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:85,103,135,237,250,273,294/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 67.3%; Score 33; DB 2; Length 298;
Best Local Similarity 100.0%; Pred. No. 5.2e-28;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KPNDPHEVFNVPVCSGNNPTCWAICKRIP 42
DB 158 KPNDPHEVFNVPVCSGNNPTCWAICKRIP 190
|||||

RESULT 10
MGNZ16
major surface glycoprotein G - human respiratory syncytial virus (strain 18537)
C:Species: human respiratory syncytial virus
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
C:Accession: B32703
R:Johnson, P.R.; Striggs, M.K.; Olmsted, R.A.; Collins, P.L.
Proc. Natl. Acad. Sci. U.S.A. 84, 5625-5629, 1987
A>Title: The G glycoprotein of human respiratory syncytial virus of subgroups A and B
A:Reference number: A32703; MUID:87289657
A:Accession: B32703
A:Molecule type: mRNA
A:Residues: 1-292 <JOH>
A:Cross-references: GB:M17213; NID:g333942; PIDN:AAA47412.1; PID:g333943
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:41-63/Domain: transmembrane #status predicted <TMN>
F:81,86,100/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 26.5%; Score 13; DB 1; Length 292;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 HEEVFNVPVCSIC 28
DB 164 HEEVFNVPVCSIC 176
|||||

RESULT 11
MGNZ60
major surface glycoprotein G - human respiratory syncytial virus (strain 8/60)
N:Alternate names: attachment glycoprotein G
C:Species: human respiratory syncytial virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C:Accession: A37077
R:Sullender, W.M.; Anderson, K.; Wertz, G.W.
Virology 178, 195-203, 1990
A>Title: The respiratory syncytial virus subgroup B attachment glycoprotein: analysis of
gous subgroup virus challenge.
A:Reference number: A37077; MUID:90357765
A:Accession: A37077
A:Molecule type: mRNA
A:Residues: 1-292 <SUL>
A:Cross-references: EMBL:M55633; NID:g333944; PIDN:AAA47413.1; PID:g333945
C:Genetics:
A:Gene: G
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:45-63/Domain: transmembrane #status predicted <TMN>
F:81,86,100,230,290/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 26.5%; Score 13; DB 1; Length 292;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 HEEVFNVPVCSIC 28
DB 164 HEEVFNVPVCSIC 176
|||||

RESULT 12
B44213
structural polyprotein - Venezuelan equine encephalitis virus (strain P676)
N:Contains: 6K protein; coat protein; membrane glycoprotein E1; membrane glycoprotein
C:Species: Venezuelan equine encephalitis virus
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999
C:Accession: B44213
R:Kinney, R.M.; Tsuchiya, K.R.; Snelder, J.M.; Trent, D.W.
Virology 191, 569-580, 1992
A>Title: Genetic evidence that epizootic Venezuelan equine encephalitis (VEE) viruses
A:Reference number: A44213; MUID:93079859
A:Accession: B44213
A:Molecule type: genomic RNA
A:Residues: 1-1255 <KIN>
A:Cross-references: GB:L04653; NID:g290609; PIDN:AAC19319.1; PID:g290611
C:Superfamily: togavirus structural polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-275/Product: coat protein #status predicted <CTP>
F:276-334/Product: membrane glycoprotein E3 #status predicted <MG3>
F:335-757/Product: membrane glycoprotein E2 #status predicted <MG2>
F:702-722/Domain: transmembrane #status predicted <TM1>
F:758-813/Product: 6K protein #status predicted <KP6>
F:793-814/Domain: transmembrane #status predicted <TM2>
F:814-1255/Product: membrane glycoprotein E1 #status predicted <MG1>
F:1232-1249/Domain: transmembrane #status predicted <TM3>
F:47,286,652,947/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.3%; Score 7; DB 1; Length 1255;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 PNKPKGK 48
DB 108 PNKPKGK 114
|||||

RESULT 13
T05672
hypothetical protein F22I13.210 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
C:Accession: T05672
R:Bevan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mayer,
submitted to the Protein Sequence Database, February 1999
A:Reference number: 215420
A:Accession: T05672
A:Molecule type: DNA
A:Residues: 1-1468 <BEV>
A:Cross-references: EMBL:AL035539
A:Experimental source: cultivar Columbia; BAC clone F22I13
C:Genetics:
A:Map position: 4
A:Introns: 65/3; 346/1; 384/3; 440/2; 475/3; 562/3; 625/3; 1339/3; 1409/3
A>Note: F22I13.210

Query Match 14.3%; Score 7; DB 2; Length 1468;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NKPPSKP 11

Db 32 NKPPSKP 38
|||||||

RESULT 14

D34047
Stylar glycoprotein 7 - Persian tobacco (fragment)
C:Species: Nicotiana glauca (Persian tobacco)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 13-Mar-1997
C:Accession: D34047
R:Jahnen, W.; Ward, L.D.; Reid, G.E.; Moritz, R.L.; Simpson, R.J.
Biochem. Biophys. Res. Commun. 166, 139-145, 1990
A:Title: Internal amino acid sequencing of proteins by in situ cyanogen bromide cleavage
A:Reference number: A90157; MUID:90147691
A:Accession: D34047
A:Molecule type: protein
A:Residues: 1-23 <JA4>
C:Superfamily: Enterobacter ribonuclease
C:Keywords: angiosperm reproduction; glycoprotein

Query Match 12.2%; Score 6; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 KRIPNK 44
|||||||
Db 17 KRIPNK 22

RESULT 15

S69116
fibrinogen gamma chain - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Mar-1998 #sequence_revision 24-Apr-1998 #text_change 02-Jul-1998
C:Accession: S69116
R:Litvinovich, S.V.; Henschen, A.H.; Krieglstein, K.G.; Ingham, K.C.; Medved, L.V.
Eur. J. Biochem. 229, 605-614, 1995
A:Title: Structural and functional characterization of proteolytic fragments derived from
A:Reference number: S69114; MUID:95278210
A:Accession: S69116
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-92 <LIT>
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology

Query Match 12.2%; Score 6; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PSKPNN 13
|||||||
Db 12 PSKPNN 17

Search completed: May 21, 2001, 14:18:17
Job time: 95 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 21, 2001, 14:17:57 ; Search time 8.3 seconds
(without alignments)
202.231 Million cell updates/sec

Title: US-09-202-035-1

Perfect score: 49

Sequence: 1 KORQKPSKPNDFEVEF.....NNPTCAICKRIPNKKPGK 49

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 93435 seqs, 34255486 residues

Word size : 0

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	49	100.0	298	1 VGLG_HRSVA	P03423 human respi
2	48	98.0	297	1 VGLG_HRSV2	P27021 human respi
3	48	98.0	297	1 VGLG_HRSV3	P27022 human respi
4	40	81.6	297	1 VGLG_HRSV4	P27023 human respi
5	40	81.6	297	1 VGLG_HRSV6	P27025 human respi
6	40	81.6	298	1 VGLG_HRSVL	P20895 human respi
7	35	71.4	297	1 VGLG_HRSV7	P27026 human respi
8	33	67.3	298	1 VGLG_HRSV5	P27024 human respi
9	13	26.5	292	1 VGLG_HRSV1	P20896 human respi
10	13	26.5	292	1 VGLG_HRSV8	P23041 human respi
11	7	14.3	1255	1 POLS_EEVVP	P36332 venezuelan
12	6	12.2	126	1 RS13_STRCO	O86773 streptomyc
13	6	12.2	126	1 Y021_CAEEL	P34671 caenorhabdi
14	6	12.2	159	1 RAC3_HUMAN	O14658 homo sapien
15	6	12.2	212	1 Y010_MYCPN	P75099 mycoplasma
16	6	12.2	218	1 Y010_MYCPE	P47256 mycoplasma
17	6	12.2	278	1 RT09_YEAST	P38120 saccharomyc
18	6	12.2	301	1 YAB4_SCHPO	O09806 schizosacch
19	6	12.2	413	1 IDHC_SOYBN	O06197 glycine max
20	6	12.2	444	1 FIBG_BOVIN	P12799 bos taurus
21	6	12.2	468	1 PCOL_RAT	O08628 rattus norv
22	6	12.2	508	1 SPA2_STAAU	P38507 staphylococ
23	6	12.2	524	1 SPAL_STAAU	P02976 staphylococ
24	6	12.2	544	1 SYFB_SULSO	P95960 sulfolobus
25	6	12.2	582	1 CIKG_HUMAN	O03721 homo sapien
26	6	12.2	615	1 COX1_BACP3	P16262 bacillus ps
27	6	12.2	625	1 CIKG_RAT	O63734 rattus norv
28	6	12.2	631	1 XRC1_MOUSE	Q60596 mus musculu
29	6	12.2	1254	1 POLS_EEVV8	P05674 venezuelan
30	6	12.2	1254	1 POLS_EEVVE	P36330 venezuelan
31	6	12.2	1254	1 POLS_EEVVM	P36331 venezuelan
32	6	12.2	1254	1 POLS_EEVVT	P09592 venezuelan
33	6	12.2	1255	1 POLS_EEVV3	P36329 venezuelan

34	6	12.2	1273	1 YAR2_SCHPO	Q10135 schizosacch
35	6	12.2	1651	1 VIT6_CAEEL	P18948 caenorhabdi
36	6	12.2	1896	1 RPBI_DROME	P04052 drosophila
37	5	10.2	74	1 SOK_ECOLI	P13971 escherichia
38	5	10.2	75	1 ULL1_EBV	P03216 Epstein-Bar
39	5	10.2	94	1 IHFB_BUCAI	P57394 buchnera ap
40	5	10.2	96	1 XYO1_HUMAN	P23262 homo sapien
41	5	10.2	101	1 FXC2_RAT	Q63246 rattus norv
42	5	10.2	103	1 CHLB_LYCAN	P37847 lycopodium
43	5	10.2	103	1 CHLB_LYCCO	P37848 lycopodium
44	5	10.2	103	1 CHLB_SELMO	P37856 selaginella
45	5	10.2	104	1 RL36_CAEEL	P49181 caenorhabdi
46	5	10.2	112	1 SPAM_SHIFL	P40708 shigella fl
47	5	10.2	116	1 GLHA_CLAGA	P53542 clarifas gar
48	5	10.2	116	1 GLHA_ICTPU	Q9Y9P3 ictalurus p
49	5	10.2	120	1 VP3_CAV26	P54095 chicken ane
50	5	10.2	121	1 VP3_CAV82	P54096 chicken ane
51	5	10.2	121	1 VP3_CAVC1	Q99152 chicken ane
52	5	10.2	121	1 VP3_CAVC1	P54094 chicken ane
53	5	10.2	125	1 ACPS_ECOLI	P24224 escherichia
54	5	10.2	125	1 YCX1_GUTHH	O78420 guillardia
55	5	10.2	136	1 Y16K_CSMV	P18919 chloris str
56	5	10.2	144	1 YV05_METJA	Q60304 methanococ
57	5	10.2	147	1 NIFU_BACSU	Q32163 bacillus su
58	5	10.2	151	1 UBC2_NEUCR	P52493 neurospora
59	5	10.2	158	1 RS31_CAEEL	Q09368 caenorhabdi
60	5	10.2	159	1 RS11_MAIZE	P25460 zea mays (m
61	5	10.2	160	1 E13J_TOBAC	P52397 nicotiana t
62	5	10.2	173	1 PRL1_MEDFR	Q40374 medicago tr
63	5	10.2	180	1 PAAD_THERAC	Q9hj72 thermoplas
64	5	10.2	180	1 Y16A_MYCMY	Q50239 mycoplasma
65	5	10.2	182	1 PAAD_ARCFU	Q29054 archaeoglob
66	5	10.2	190	1 GCH1_CAMJE	P51594 campylobact
67	5	10.2	191	1 LEUD_LACLA	Q02144 lactococcus
68	5	10.2	194	1 YQ03_CAEEL	Q09294 caenorhabdi
69	5	10.2	196	1 YEL9_YEAST	P40018 saccharomyc
70	5	10.2	198	1 RECR_STRPN	Q9zhc4 streptococ
71	5	10.2	200	1 SYST_LYCES	P27058 lycopersico
72	5	10.2	201	1 YADL_ECOLI	P37017 escherichia
73	5	10.2	202	1 NUKM_TRYBB	Q26783 trypanosoma
74	5	10.2	203	1 RB13_HUMAN	P51153 homo sapien
75	5	10.2	204	1 IPP2_RABIT	P11845 oryctolagus
76	5	10.2	205	1 POLG_CXA23	P08490 coxsackievi
77	5	10.2	205	1 YICG_ECOLI	P31432 escherichia
78	5	10.2	206	1 YCX1_CYAPA	P48323 cyanophora
79	5	10.2	209	1 YIL3_YEAST	P40479 saccharomyc
80	5	10.2	211	1 YFDX_ECOLI	P76520 escherichia
81	5	10.2	213	1 CGB1_MEDSA	P30286 medicago sa
82	5	10.2	213	1 GCHI_OSTOS	O61573 ostertagia
83	5	10.2	213	1 RB25_HUMAN	P57735 homo sapien
84	5	10.2	217	1 H1_ANAPL	P09426 anas platyr
85	5	10.2	217	1 H1_CHICK	P09887 gallus gall
86	5	10.2	218	1 H101_CHICK	P08284 gallus gall
87	5	10.2	219	1 YB87_ARATH	O81004 arabidopsis
88	5	10.2	219	1 YOFA_ECOLI	Q46827 escherichia
89	5	10.2	220	1 FGF3_CHICK	P48801 gallus gall
90	5	10.2	223	1 GCH1_CAEEL	P19980 caenorhabdi
91	5	10.2	224	1 T2V1_BACST	P43421 bacillus st
92	5	10.2	225	1 RU2B_HUMAN	P08579 homo sapien
93	5	10.2	225	1 TPIS_PYRMO	P95583 pyrococcus
94	5	10.2	229	1 NISR_LACLA	Q07597 lactococcus
95	5	10.2	229	1 VIF_CAEVC	P33462 caprine art
96	5	10.2	229	1 VV_PI4HA	P21739 human parai
97	5	10.2	229	1 Y467_BORBU	O51423 borrelia bu
98	5	10.2	231	1 TPIS_PYRBU	O59536 pyrococcus
99	5	10.2	235	1 C554_NITEU	Q37142 nitrosomona
100	5	10.2	236	1 CD81_CERAE	P37703 cercopithe
101	5	10.2	236	1 CD81_HUMAN	P18582 homo sapien
102	5	10.2	236	1 CD81_MOUSE	P35762 mus musculu
103	5	10.2	236	1 CD81_RAT	Q62745 rattus norv
104	5	10.2	238	1 ET3_HUMAN	P14138 homo sapien
105	5	10.2	243	1 GCHI_YEAST	P51601 saccharomyc
106	5	10.2	246	1 RS3_DROME	Q06559 drosophila

107	1	10.2	247	1	MCT1_HUMAN	P23946	homo sapien	180	379	1	5H1D_FUGRU	P79748	fugu rubrip
108	1	10.2	247	1	MCT1_MACFA	P56435	macaca fasc	181	379	1	CYBA_STELO	P24962	stenella lo
109	1	10.2	247	1	MCT1_PAPHA	P52195	papio hamad	182	379	1	CYBE_STELO	P24963	stenella lo
110	1	10.2	249	1	MCT1_CANFA	P21842	canis famil	183	379	1	CYB_ALCAA	O47922	alces alces
111	1	10.2	251	1	Y4EF_RHNSN	P55429	rhizobium s	184	379	1	CYB_AMMLE	P78781	ammotragus
112	1	10.2	253	1	S40B_CHITE	Q05019	chironomus	185	379	1	CYB_ANTAM	P24992	antilocapra
113	1	10.2	253	1	VG23_HSVSA	Q01006	herpesvirus	186	379	1	CYB_ARTAD	O95719	artibeus an
114	1	10.2	260	1	NADE_HELPJ	Q92mb0	helicobacte	187	379	1	CYB_ARTAZ	O95718	artibeus az
115	1	10.2	260	1	NADE_HELPJ	O25096	helicobacte	188	379	1	CYB_ARTCI	O95723	artibeus ci
116	1	10.2	268	1	SET_DROME	P53997	drosofila	189	379	1	CYB_ARTFI	O95723	artibeus co
117	1	10.2	270	1	YKAA_CAEEL	P13451	caenorhabdi	190	379	1	CYB_ARTFI	O95728	artibeus fi
118	1	10.2	273	1	IE68_HSVEA	P18346	equine herp	191	379	1	CYB_ARTFI	O95727	artibeus fi
119	1	10.2	275	1	E131_TOBAC	P52396	nicotiana t	192	379	1	CYB_ARTFR	O95731	artibeus fr
120	1	10.2	278	1	L1L1_MOUSE	P27792	mus musculu	193	379	1	CYB_ARTGA	O95731	artibeus gl
121	1	10.2	279	1	DAPE_AQUAE	O67693	aquifex aeo	194	379	1	CYB_ARTGG	O95729	artibeus gl
122	1	10.2	281	1	CD37_MOUSE	Q61470	mus musculu	195	379	1	CYB_ARTGW	O95730	artibeus gl
123	1	10.2	281	1	CD37_MOUSE	P13053	rattus norv	196	379	1	CYB_ARTHA	O95734	artibeus ha
124	1	10.2	285	1	GSPC_KLEPN	P15643	klebsiella	197	379	1	CYB_ARTHI	O95735	artibeus hi
125	1	10.2	286	1	CH36_DROME	P07182	drosofila	198	379	1	CYB_ARTIO	O95737	artibeus in
126	1	10.2	291	1	NULM_CAEEL	P24887	caenorhabdi	199	379	1	CYB_ARTIT	O95736	artibeus in
127	1	10.2	292	1	METF_HAEIN	P45208	haemophilus	200	379	1	CYB_ARTJA	O95738	artibeus ja
128	1	10.2	292	1	RT09_KLUMA	Q9p4c1	kluyveromyc	201	379	1	CYB_ARTLI	O95739	artibeus li
129	1	10.2	292	1	SUB1_YEAST	P54000	saccharomyc	202	379	1	CYB_ARTPH	O95741	artibeus ob
130	1	10.2	293	1	CH36_DROVI	P17111	drosofila	203	379	1	CYB_ARTPL	O95744	artibeus ph
131	1	10.2	294	1	DRAG_RHORI	P14300	rhodospirill	204	379	1	CYB_ARTTL	O95745	artibeus pl
132	1	10.2	298	1	JAMI_BOVIN	Q9xt56	bos taurus	205	379	1	CYB_ASTPE	O33818	asterina pe
133	1	10.2	299	1	JAMI_HUMAN	O9V624	homo sapien	206	379	1	CYB_BALBN	P1280	balaeonopter
134	1	10.2	300	1	CD38_HUMAN	O88907	homo sapien	207	379	1	CYB_BALBN	P1281	balaeonopter
135	1	10.2	300	1	JAMI_MOUSE	O88792	mus musculu	208	379	1	CYB_BALBO	P41282	balaeonopter
136	1	10.2	302	1	MOVP_CCMV	P20180	cowpea chlo	209	379	1	CYB_BALGL	P41283	balaeonopter
137	1	10.2	305	1	OPPC_BACSU	P24139	bacillus su	210	379	1	CYB_BALGL	P41284	balaeonopt
138	1	10.2	309	1	YJ53_YEAST	P47129	saccharomyc	211	379	1	CYB_BALMU	P41284	balaeonopt
139	1	10.2	310	1	YCYJ_ECOLI	P76049	escherichia	212	379	1	CYB_BALMY	P41286	balaeonopt
140	1	10.2	310	1	YIHG_ECOLI	P32129	escherichia	213	379	1	CYB_BALPH	P41286	balaeonopt
141	1	10.2	316	1	BLA3_BACCE	O65548	bacillus ce	214	379	1	CYB_BEAPH	P24950	balaeonopt
142	1	10.2	319	1	A33_HUMAN	O99795	homo sapien	215	379	1	CYB_BOVIN	O47420	beatragus h
143	1	10.2	319	1	YB98_MYCPN	Q50290	mycoplasma	216	379	1	CYB_CAMBA	P00157	bos taurus
144	1	10.2	320	1	CH36_CERCA	P17110	ceratitis c	217	379	1	CYB_CAMDR	O34028	camelus bac
145	1	10.2	322	1	YS53_CAEEL	O93377	caenorhabdi	218	379	1	CYB_CAPAE	P24952	camelus dro
146	1	10.2	323	1	Y495_MYCLE	P54579	mycobacteri	219	379	1	CYB_CAPAE	O78788	capra cauca
147	1	10.2	324	1	LUXB_VIBHA	P07739	vibrio harv	220	379	1	CYB_CAPCY	O78787	capra cylin
148	1	10.2	325	1	BIRA_BACSU	P42975	bacillus su	221	379	1	CYB_CAPHI	O78786	capra falco
149	1	10.2	325	1	CTH1_YEAST	P47976	saccharomyc	222	379	1	CYB_CAPHI	P24953	capra hircu
150	1	10.2	325	1	MODD_MYCBO	O30620	mycobacteri	223	379	1	CYB_CAPMB	O78785	capra ibex
151	1	10.2	325	1	MODD_MYCBO	Q05096	mycobacteri	224	379	1	CYB_CAPMB	P41287	caperea mar
152	1	10.2	325	1	RPOA_MYCTU	Q91rdv6	mycoplasma	225	379	1	CYB_CAPNU	O78790	capra nubia
153	1	10.2	331	1	E13K_TOBAC	P52398	nicotiana t	226	379	1	CYB_CAPNU	O47926	capreolus p
154	1	10.2	331	1	SRA1_CAEEL	O93203	caenorhabdi	227	379	1	CYB_CEREL	O47924	cervus elap
155	1	10.2	333	1	Y244_METJA	O60299	methanococc	228	379	1	CYB_CERNI	Q34172	cervus nipp
156	1	10.2	333	1	OAC_BPSF6	P23214	bacterioph	229	379	1	CYB_CONTA	O47421	connochaete
157	1	10.2	336	1	RF09_CANAL	O94150	candida alb	230	379	1	CYB_DAMDA	P24955	dama dama
158	1	10.2	337	1	VF11_VACCP	P29888	vaccinia vi	231	379	1	CYB_DASNO	O21337	dasyptus nov
159	1	10.2	338	1	RFPG_HAEIN	P44914	haemophilus	232	379	1	CYB_DELEL	O03812	deiphinapte
160	1	10.2	343	1	E13G_TOBAC	P23547	nicotiana t	233	379	1	CYB_DUGDU	Q33401	dugong dugo
161	1	10.2	347	1	TOLA_PSEAE	P50600	pseudomonas	234	379	1	CYB_ERIEU	Q36368	erinaeace e
162	1	10.2	347	1	YDJJ_ECOLI	P77280	escherichia	235	379	1	CYB_ESCGI	P41288	eschrichtiu
163	1	10.2	350	1	NTRB_VIBAL	P19906	vibrio algi	236	379	1	CYB_GAZGA	O48336	gazella gaz
164	1	10.2	351	1	CAV2_CAEEL	Q18879	caenorhabdi	237	379	1	CYB_HEMJE	O78783	hemitragus
165	1	10.2	351	1	P53_ORYLA	P79820	oryzias lat	238	379	1	CYB_HYDLN	O47930	hydropotes
166	1	10.2	356	1	E13L_TOBAC	P52399	nicotiana t	239	379	1	CYB_LAMGL	Q34891	lama glama
167	1	10.2	357	1	TGN3_RAT	P19814	rattus norv	240	379	1	CYB_LAMPA	Q34916	lama guanic
168	1	10.2	358	1	Y502_MYCTU	Q11167	mycobacteri	241	379	1	CYB_LAMVI	Q36227	lama vicugn
169	1	10.2	359	1	ALF_BORBU	O51401	borrelia bu	242	379	1	CYB_MEGNO	P41289	megaptera n
170	1	10.2	361	1	HEM3_HUMAN	P08397	homo sapien	243	379	1	CYB_MONMO	P92657	monodon mon
171	1	10.2	361	1	HEM3_MOUSE	P22907	mus musculu	244	379	1	CYB_MOSLE	O47584	moschus leu
172	1	10.2	367	1	HEM3_RAT	P19356	rattus norv	245	379	1	CYB_MOSMO	P24960	moschus mos
173	1	10.2	367	1	Y502_MYCLE	P54878	mycobacteri	246	379	1	CYB_ODOHE	O78778	odocoileus
174	1	10.2	368	1	TRPC_ARATH	P49572	arabidopsis	247	379	1	CYB_OVIDA	O78779	ovis ammon
175	1	10.2	370	1	P2C2_SCHPO	Q09172	schizosacch	248	379	1	CYB_OVIVV	O78780	ovis vignei
176	1	10.2	372	1	AGL1URTDI	P11218	urtica dioi	249	379	1	CYB_PHOGR	Q35457	phoca groen
177	1	10.2	373	1	GLNA_MOUSE	P15105	mus musculu	250	379	1	CYB_PHOPH	O03811	phocoenoid
178	1	10.2	376	1	KDCB_DROME	P16911	drosofila	251	379	1			
179	1	10.2	378	1	BI0B_ARATH	P54967	arabidopsis	252	379	1			

253 10.2 379 1 CYB_PHYCA P41290 physeter ca
254 5 10.2 379 1 CYB_PIG P24964 mus scrofa
255 5 10.2 379 1 CYB_PSENA O78782 pseudis na
256 5 10.2 379 1 CYB_RABIT P34863 oryctolagus
257 5 10.2 379 1 CYB_SHEEP P24959 ovis aries
258 5 10.2 379 1 CYB_SIGLI O47419 sigmocer
259 5 10.2 379 1 CYB_STEAT P24961 stenella at
260 5 10.2 379 1 CYB_TAYTA P24966 tayassu taj
261 5 10.2 379 1 CYB_TRANA P24965 tragus na
262 5 10.2 380 1 COAT_CNV P15183 cucumer ne
263 5 10.2 380 1 CYB_ACITR P11669 acipenser t
264 5 10.2 380 1 CYB_CAPSI O78784 capra sibir
265 5 10.2 380 1 CYB_GADMO O37080 gadus morhu
266 5 10.2 380 1 CYB_LATCH O03176 latimeria c
267 5 10.2 380 1 CYB_MICAR O36922 microtus ar
268 5 10.2 380 1 CYB_MICLO P56731 microtus lo
269 5 10.2 380 1 CYB_PELSU O79680 pelomedusa
270 5 10.2 380 1 CYB_RAT P00159 rattus norv
271 5 10.2 380 1 CYB_RUPPY O78777 rupicapra p
272 5 10.2 381 1 CYB_ANTLE O63537 antechinus
273 5 10.2 381 1 CYB_ANTNA Q33800 antechinus
274 5 10.2 381 1 CYB_DASRO Q34376 dasykaluta
275 5 10.2 381 1 CYB_MOUSE P00158 mus musculu
276 5 10.2 381 1 CYB_MURLO Q35020 murexia lon
277 5 10.2 381 1 CYB_MYOME Q35038 myoictis me
278 5 10.2 382 1 CYB_MONDO O04911 monodelphis
279 5 10.2 383 1 TRML_PYRAB Q9vlp3 pyrococcus
280 5 10.2 385 1 CYB_SACDO Q35819 saccharomyc
281 5 10.2 385 1 CYB_YEAST P00163 saccharomyc
282 5 10.2 396 1 O45E_DROME Q9v589 drosophila
283 5 10.2 397 1 RKQP_CAEEL P34303 caenorhabdi
284 5 10.2 399 1 RRBP_P14HA P22044 human parai
285 5 10.2 402 1 YJF3_YEAST P39542 saccharomyc
286 5 10.2 405 1 YJF2_YEAST P38746 saccharomyc
287 5 10.2 411 1 YAL2_SCHPO Q09685 schizosacch
288 5 10.2 413 1 CRF2_XENLA O42603 xenopus lae
289 5 10.2 416 1 CREA_EMENI Q01981 emericella
290 5 10.2 420 1 CLPX_CHLTR O84711 chlamydia t
291 5 10.2 420 1 CAQS_RANES P31231 rana escul
292 5 10.2 420 1 GLYA_ACTAC P34894 actinobacil
293 5 10.2 421 1 GLYA_HAETIN P43844 haemophilus
294 5 10.2 422 1 YF2L_MERJA Q58916 methanococc
295 5 10.2 424 1 V54E_TBRSV P22051 tomato blac
296 5 10.2 427 1 CREA_ASPNG Q05620 aspergillus
297 5 10.2 428 1 CG1B_MEDVA P46277 medicago va
298 5 10.2 431 1 CREA_ASPAC O94166 aspergillus
299 5 10.2 431 1 YAZ1_SCHPO Q10223 schizosacch
300 5 10.2 435 1 PEPC_LACILC Q04723 lactococcus
301 5 10.2 438 1 HVC2_HETFR P23085 heterodontu
302 5 10.2 443 1 HXA3_HUMAN O43365 homo sapien
303 5 10.2 448 1 SRF_XENLA P23790 xenopus lae
304 5 10.2 451 1 GAA2_BOVIN P10063 bos taurus
305 5 10.2 451 1 GAA2_HUMAN P47869 homo sapien
306 5 10.2 451 1 GAA2_MOUSE P26048 mus musculu
307 5 10.2 451 1 GAA2_RAT P23576 rattus norv
308 5 10.2 454 1 YUAE_CAEEL P52715 caenorhabdi
309 5 10.2 455 1 NCBI_MOUSE Q02819 mus musculu
310 5 10.2 456 1 RINI_RAT P29315 rattus norv
311 5 10.2 457 1 YM59_YEAST Q03648 saccharomyc
312 5 10.2 461 1 KDTA_RICPR Q9ze58 rickettsia
313 5 10.2 466 1 CRD1_ANAPL P24057 anas platyr
314 5 10.2 466 1 CRD1_ANSAN P33110 anser anser
315 5 10.2 468 1 CRD2_ANAPL P24058 anas platyr
316 5 10.2 472 1 POU2_BRARE Q90270 brachydanio
317 5 10.2 472 1 YWIE_CAEEL Q23525 caenorhabdi
318 5 10.2 476 1 GREI_BALAM Q93126 balanus amp
319 5 10.2 482 1 YJQ2_YEAST P46997 saccharomyc
320 5 10.2 484 1 Y130_MYCGE P47376 mycoplasma
321 5 10.2 485 1 ER24_FUSSO Q01447 fusarium so
322 5 10.2 487 1 HH1R_HUMAN P35367 homo sapien
323 5 10.2 488 1 HH1R_MOUSE P70174 mus musculu
324 5 10.2 491 1 HH1R_BOVIN P30546 bos taurus
325 5 10.2 493 1 UGDH_MOUSE O70475 mus musculu

326 5 10.2 493 1 UGDH_RAT O70199 rattus norv
327 5 10.2 494 1 FXC2_MOUSE Q61850 mus musculu
328 5 10.2 494 1 UGDH_BOVIN P12378 bos taurus
329 5 10.2 494 1 UGDH_HUMAN O60701 homo sapien
330 5 10.2 496 1 NIFE_RHISN P55673 rhizobium s
331 5 10.2 496 1 NOS2_RABIT O19114 oryctolagus
332 5 10.2 498 1 IL14_HUMAN P40222 homo sapien
333 5 10.2 501 1 FXC2_HUMAN Q99958 homo sapien
334 5 10.2 501 1 LCYB_ARATH Q38933 arabidopsis
335 5 10.2 501 1 NRFL_HUMAN Q16656 homo sapien
336 5 10.2 503 1 NRFL_MOUSE Q9u000 mus musculu
337 5 10.2 504 1 ENGA_HAETIN P44536 haemophilus
338 5 10.2 504 1 Y4JA_RHISN P55501 rhizobium s
339 5 10.2 506 1 UDPG_SCHPO P78811 schizosacch
340 5 10.2 507 1 CHLB_PORPU P51278 porphyra pu
341 5 10.2 508 1 CROC_DROME P32027 drosophila
342 5 10.2 508 1 SRF_HUMAN P11831 homo sapien
343 5 10.2 508 1 VLL_HPVG O50821 human papil
344 5 10.2 508 1 Y736_HAETIN P44849 haemophilus
345 5 10.2 509 1 C4AI_DROME Q9vms9 drosophila
346 5 10.2 509 1 DHAC_CHICK P27463 gallus gall
347 5 10.2 510 1 ATPA_BUCAP O51874 buchera ap
348 5 10.2 512 1 ATPA_BUCAI P57122 buchera ap
349 5 10.2 517 1 Z215_HUMAN Q9u158 homo sapien
350 5 10.2 518 1 PR31_SCHPO O42504 schizosacch
351 5 10.2 526 1 HRG_RABIT Q28640 oryctolagus
352 5 10.2 527 1 YEGH_ECOLI P76389 escherichia
353 5 10.2 529 1 IMA2_HUMAN P52292 homo sapien
354 5 10.2 537 1 TEE6_STRPY P18481 streptococc
355 5 10.2 540 1 YMA5_CAEEL P34450 caenorhabdi
356 5 10.2 541 1 PRPR_SALTY P74839 salmonella
357 5 10.2 541 1 AGM1_CANAL Q9p4v2 candida alb
358 5 10.2 550 1 YL00_MYCTU Q10709 mycobacteri
359 5 10.2 553 1 FXCL_HUMAN Q12948 homo sapien
360 5 10.2 553 1 FXCL_MOUSE O61572 mus musculu
361 5 10.2 556 1 PPBD_BACSU P42251 bacillus su
362 5 10.2 561 1 YGG4_YEAST P53166 saccharomyc
363 5 10.2 565 1 VNUC_INCCA P08028 influenza c
364 5 10.2 566 1 Y397_MYCGE P37637 mycoplasma
365 5 10.2 577 1 G6PC_SOLTU Q43839 solanum tub
366 5 10.2 582 1 TNPA_BACFR O45119 bacteroides
367 5 10.2 585 1 ASN1_LOTJA P49092 lotus japon
368 5 10.2 585 1 ASN1_PEA P19251 pisum sativ
369 5 10.2 585 1 YAOH_SCHPO Q10096 schizosacch
370 5 10.2 587 1 NDC2_RAT P70545 rattus norv
371 5 10.2 589 1 ASNS_ASPOF P31752 asparagus o
372 5 10.2 592 1 NDC1_HUMAN Q13183 homo sapien
373 5 10.2 603 1 SNTD_HAETIN P44569 haemophilus
374 5 10.2 605 1 RTK2_GEOCY P42159 geodia cydo
375 5 10.2 609 1 HSF_SCHPO Q02953 schizosacch
376 5 10.2 610 1 CDP1_ARATH Q06850 arabidopsis
377 5 10.2 619 1 M3K2_MOUSE Q61083 mus musculu
378 5 10.2 622 1 YAE7_YEAST P39723 saccharomyc
379 5 10.2 623 1 NRC2_NEUCR O42626 neurospora
380 5 10.2 628 1 DP19_CAEEL P34413 caenorhabdi
381 5 10.2 632 1 FMN2_HUMAN Q9nz56 homo sapien
382 5 10.2 639 1 NRG1_HUMAN Q02297 h pro-neure
383 5 10.2 644 1 YED0_YEAST P39987 saccharomyc
384 5 10.2 648 1 PIG1_YEAST Q06216 saccharomyc
385 5 10.2 654 1 PSTA_MYCGE P47651 mycoplasma
386 5 10.2 662 1 NRG1_RAT P43322 r pro-neure
387 5 10.2 667 1 KJF7_YEAST P47042 saccharomyc
388 5 10.2 674 1 TML1_ARATH P33543 arabidopsis
389 5 10.2 682 1 YEB9_METJA Q58884 methanococc
390 5 10.2 687 1 VS41_GIALA P92127 giardia lam
391 5 10.2 688 1 CHLB_CHLRE P36437 chlamydomon
392 5 10.2 689 1 GALX_PACTA Q40801 pachysolen
393 5 10.2 689 1 YE30_HELPY P56185 helicobacte
394 5 10.2 691 1 PP21_YEAST P26570 saccharomyc
395 5 10.2 692 1 YE30_HELPJ Q9zj16 helicobacte
396 5 10.2 697 1 Y441_HUMAN Q43167 homo sapien
397 5 10.2 702 1 ADA3_YEAST P32494 saccharomyc
398 5 10.2 704 1 CDGT_BACOH P27036 bacillus oh

399	5	10.2	707	1	SFPQ_HUMAN	P23246	homo sapien	472	5	10.2	1221	1	UBP2_KLUJIA	O42726	kluyveromyc	
400	5	10.2	710	1	CDGT_THETU	P26827	thermoanaer	473	5	10.2	1230	1	ST20_CANAL	Q92212	candida ali	
401	5	10.2	715	1	VGL_SVP1R	P15892	spiroplasma	474	5	10.2	1253	1	POLS_SFV	P03315	semliki for	
402	5	10.2	718	1	CDGT_BACCI	P30920	bacillus ci	475	5	10.2	1270	1	DYNA_HUMAN	Q14203	homo sapien	
403	5	10.2	718	1	CDGT_BACCI	P14014	bacillus li	476	5	10.2	1270	1	UBP2_YEAST	Q01476	saccharomyc	
404	5	10.2	718	1	CDGT_BACSS	P31747	bacillus sp	477	5	10.2	1280	1	DYNA_RAT	P28023	rattus norv	
405	5	10.2	722	1	Y174_RICPR	P81171	rickettsia	478	5	10.2	1281	1	DYNA_MOUSE	O08788	mus musculus	
406	5	10.2	746	1	EXTL1_HUMAN	Q16394	homo sapien	479	5	10.2	1322	1	YAG3_YEAST	P39712	saccharomyc	
407	5	10.2	746	1	EXTL1_MOUSE	P97464	mus musculus	480	5	10.2	1328	1	POLX_TOBAC	P10978	nicotiana t	
408	5	10.2	773	1	ITB1_BOVIN	P53712	bos taurus	481	5	10.2	1356	1	KAB7_YEAST	P31374	saccharomyc	
409	5	10.2	788	1	ACON_CAEEL	P34455	caenorhabdi	482	5	10.2	1380	1	ZMS1_YEAST	P46974	saccharomyc	
410	5	10.2	793	1	S3AI_HUMAN	P15459	homo sapien	483	5	10.2	1390	1	INSR_AEDAE	Q33105	aedes aegyp	
411	5	10.2	798	1	ITB0_XENIA	P12607	xenopus lae	484	5	10.2	1405	1	RPC1_SCHPO	O94666	schizosacch	
412	5	10.2	798	1	ITB1_FELCA	P53713	felis silve	485	5	10.2	1419	1	MDR_PLAFA	P13568	plasmodium	
413	5	10.2	798	1	ITB1_HUMAN	P05556	homo sapien	486	5	10.2	1468	1	DPOA_YEAST	P13382	saccharomyc	
414	5	10.2	798	1	ITB1_MOUSE	P09055	mus musculus	487	5	10.2	1471	1	MYS4_YEAST	P32492	saccharomyc	
415	5	10.2	798	1	ITB1_XENIA	P12606	xenopus lae	488	5	10.2	1471	1	HTK7_HYDAT	Q25197	hydra atten	
416	5	10.2	799	1	ITB1_RAT	P49134	rattus norv	489	5	10.2	1492	1	DPOA_OXYNO	Q94636	oxytricha n	
417	5	10.2	803	1	ITB1_CHICK	P07228	gallus gall	490	5	10.2	1508	1	AT5A_MOUSE	O54827	mus muscula	
418	5	10.2	803	1	UBPE_YEAST	P38237	saccharomyc	491	5	10.2	1513	1	DPOA_OXYTR	Q27152	oxytricha t	
419	5	10.2	817	1	YGAB_YEAST	P46951	saccharomyc	492	5	10.2	1525	1	POLG_STEVM	P09732	st. louis e	
420	5	10.2	834	1	ALIM_YEAST	P03875	saccharomyc	493	5	10.2	1570	1	P3K1_DICDI	P54673	dictyosteli	
421	5	10.2	851	1	ENV_HV2DI	P17755	human immun	494	5	10.2	1603	1	VIT5_CAEEL	Q06125	caenorhabdi	
422	5	10.2	865	1	TOPI_ECOLI	P06612	escherichia	495	5	10.2	1629	1	RRPO_SHMV	P89202	sunn-hemp m	
423	5	10.2	880	1	SVF_BACST	P11931	bacillus st	496	5	10.2	1700	1	BAR3_CHITE	Q03376	chironomus	
424	5	10.2	886	1	SUHW_DROAN	Q08875	drosophila	497	5	10.2	1772	1	MSP1_PLAYO	P13828	plasmodium	
425	5	10.2	899	1	SUHW_DROVI	O08876	drosophila	498	5	10.2	1873	1	CCAS_RABIT	P07293	oryctolagus	
426	5	10.2	907	1	TREA_CANAL	P52494	candida alb	499	5	10.2	1906	1	KMLS_CHICK	P11799	gallus gall	
427	5	10.2	917	1	MSH2_DROME	P43248	drosophila	500	5	10.2	1914	1	KMLS_HUMAN	Q15746	homo sapien	
428	5	10.2	918	1	IL6B_RAT	P40190	rattus norv	501	5	10.2	1980	1	MC3A_HUMAN	Q60318	homo sapien	
429	5	10.2	919	1	YK05_YEAST	P36051	saccharomyc	502	5	10.2	1982	1	CHDM_DROME	O97159	drosophila	
430	5	10.2	923	1	RE11_SCHPO	Q92380	schizosacch	503	5	10.2	2136	1	YCF2_MARPO	P09975	marichantia	
431	5	10.2	927	1	IF2_STRAG	O94f20	streptococc	504	5	10.2	2203	1	POLG_EC09B	O66577	e genome po	
432	5	10.2	937	1	MSH2_NEUCR	O13396	neurospora	505	5	10.2	2206	1	POLG_CXA21	P22055	c genome po	
433	5	10.2	944	1	SUHW_DROME	P08970	drosophila	506	5	10.2	2206	1	POLG_POLIM	P03299	p genome po	
434	5	10.2	945	1	SVF_NEIMA	Q91x22	neisseria m	507	5	10.2	2208	1	POLH_POLIM	P03300	p genome po	
435	5	10.2	945	1	SVF_NEIMB	Q9K1h7	neisseria m	508	5	10.2	2209	1	POLG_POLIM	P03301	poliovirus	
436	5	10.2	950	1	Y136_HUMAN	Q14149	homo sapien	509	5	10.2	2214	1	POLG_CXA24	P36290	c genome po	
437	5	10.2	950	1	Y511_RICPR	Q92d36	rickettsia	510	5	10.2	2294	1	YCF2_ARATH	P56786	arabidopsis	
438	5	10.2	952	1	YK15_CAEEL	P46012	caenorhabdi	511	5	10.2	2295	1	WDR9_HUMAN	Q9ns16	homo sapien	
439	5	10.2	959	1	MSH1_YEAST	P25846	saccharomyc	512	5	10.2	2301	1	POLG_TMEVD	P13899	t genome po	
440	5	10.2	964	1	UL70_MCMVS	Q99153	murine cyto	513	5	10.2	2303	1	POLG_TMEVB	P08544	t genome po	
441	5	10.2	970	1	SU01_YEAST	P33550	saccharomyc	514	5	10.2	2303	1	POLG_TMEVG	P08545	t genome po	
442	5	10.2	976	1	PD03_YEAST	P33200	saccharomyc	515	5	10.2	2375	1	ATRX_HUMAN	P46100	homo sapien	
443	5	10.2	996	1	PIP2_YEAST	P52960	saccharomyc	516	5	10.2	2555	1	PPS3_BACSU	P39847	bacillus su	
444	5	10.2	996	1	VGNM_RCMV	P13561	red clover	517	5	10.2	3063	1	CA1C_MOUSE	Q98715	homo sapien	
445	5	10.2	1001	1	IF2_SYNY3	P72689	synecocyst	518	5	10.2	3067	1	CA1C_MOUSE	Q60847	mus musculus	
446	5	10.2	1002	1	SVIM_YEAST	P48526	saccharomyc	519	5	10.2	3176	1	CA36_HUMAN	P12111	homo sapien	
447	5	10.2	1036	1	YAN2_SCHPO	Q10068	schizosacch	520	5	10.2	3655	1	YAMB_SCHPO	Q10064	schizosacch	
448	5	10.2	1051	1	CARB_SULSO	Q59969	sulfolobus	521	5	10.2	3726	1	TRX_DROME	P20659	drosophila	
449	5	10.2	1052	1	MGPC_MYCCE	P22747	mycoplasma	522	5	10.2	4660	1	LRP2_RAT	P98158	rattus norv	
450	5	10.2	1062	1	UL70_HCMVA	P17149	human cytom	523	4	8.2	19	1	LPRM_STAAR	P03063	staphylococ	
451	5	10.2	1069	1	S24B_ARATH	Q9m081	arabidopsis	524	4	8.2	25	1	GUN1_CLOJO	P12111	clostridium	
452	5	10.2	1076	1	NUP1_YEAST	P20676	saccharomyc	525	4	8.2	25	1	PRLA_ACHLY	P27459	achromobact	
453	5	10.2	1086	1	NNTM_MOUSE	Q61941	mus musculus	526	4	8.2	27	1	CXK7_CONPU	P56633	conus purpu	
454	5	10.2	1092	1	KPBB_HUMAN	Q93100	homo sapien	527	4	8.2	36	1	NEUY_PIG	P01304	sus scrofa	
455	5	10.2	1097	1	S24C_ARATH	Q9m291	arabidopsis	528	4	8.2	36	1	NEUY_RABIT	P09640	oryctolagus	
456	5	10.2	1098	1	GRSA_BACBR	P14687	bacillus br	529	4	8.2	36	1	NEUY_RANRI	P29949	rana ridibu	
457	5	10.2	1104	1	COLA_CLOPE	P43153	clostridium	530	4	8.2	36	1	NEUY_SHEEP	P14765	ovis aries	
458	5	10.2	1144	1	NOS2_MOUSE	P29477	mus musculus	531	4	8.2	37	1	CGRP_PIG	P30880	sus scrofa	
459	5	10.2	1146	1	CCAS_RAT	Q02485	rattus norv	532	4	8.2	37	1	CGRP_PANRI	P31888	rana ridibu	
460	5	10.2	1147	1	NOS2_RAT	Q06518	rattus norv	533	4	8.2	37	1	CGRP_SHEEP	P30881	ovis aries	
461	5	10.2	1147	1	NS2D_HUMAN	O60591	homo sapien	534	4	8.2	37	1	GRP_SHEEP	P24355	astasia lon	
462	5	10.2	1169	1	Y785_RICPR	O05975	rickettsia	535	4	8.2	37	1	GRP_PANRI	P48131	cytrophora	
463	5	10.2	1187	1	PTNE_HUMAN	Q15678	homo sapien	536	4	8.2	37	1	GRP_PANRI	P56360	chlorella v	
464	5	10.2	1189	1	PTNE_MOUSE	Q82130	mus musculus	537	4	8.2	37	1	GRP_PANRI	P48131	cytrophora	
465	5	10.2	1189	1	PTC_FICPA	P78992	pichia past	538	4	8.2	37	1	GRP_PANRI	P03069	epifagus vi	
466	5	10.2	1196	1	DNBI_HSV11	P04296	herpes simp	539	4	8.2	37	1	GRP_PANRI	P12132	euglena gra	
467	5	10.2	1196	1	DNBI_HSV1F	P17469	herpes simp	540	4	8.2	37	1	GRP_PANRI	P12142	marichantia	
468	5	10.2	1196	1	DNBI_HSV1K	P17470	herpes simp	541	4	8.2	37	1	GRP_PANRI	Q94568	odontella s	
469	5	10.2	1196	1	DNBI_HSV2H	P89452	herpes simp	542	4	8.2	37	1	GRP_PANRI	P12143	oryza sativ	
470	5	10.2	1197	1	DNBI_HSV2	P36384	herpes simp	543	4	8.2	37	1	GRP_PANRI	P07815	pisum sativ	
471	5	10.2	1219	1	YH29_YEAST	Q04439	saccharomyc	544	4	8.2	37	1	GRP_PANRI	P41631	pinus thunb	
															P51296	porphyra pu

545	4	8.2	37	1	RR36_SPIOL	P12230	spinacia ol	618	4	8.2	68	1	ATX1_RAT	Q9wuc4	rattus norv
546	4	8.2	37	1	RR36_TOBAC	P12144	nicotiana t	619	4	8.2	68	1	ATX1_SHEEP	Q07633	ovis aries
547	4	8.2	37	1	RL36_AQUAE	O66487	aquifex aeo	620	4	8.2	69	1	YLA1_BACSU	O07633	capillus su
548	4	8.2	37	1	RL36_BACST	P07841	bacillus st	621	4	8.2	70	1	PSAE_CYPAP	P48114	cyanophora s
549	4	8.2	37	1	RL36_BORBU	O51452	borrelia bu	622	4	8.2	70	1	YAJM_RHLSN	P55513	rhizobium s
550	4	8.2	37	1	RL36_CAMJE	Q9pm84	campylobact	623	4	8.2	70	1	YIM6_BPPH1	P10430	bacterioph
551	4	8.2	37	1	RL36_DEIRA	Q9rsko	deinococcus	624	4	8.2	71	1	ACAL_ACALU	P81592	acalolepta
552	4	8.2	37	1	RL36_HAEIN	P46361	haemophilus	625	4	8.2	72	1	SP23_HUMAN	P22532	homo sapien
553	4	8.2	37	1	RL36_HELPJ	Q9zjtl	helicobacte	626	4	8.2	73	1	MT_DREPO	Q94550	dreissena p
554	4	8.2	37	1	RL36_HELPJ	P56058	helicobacte	627	4	8.2	73	1	RK27_CHRAL	P41549	chrysoschro
555	4	8.2	37	1	RL36_LEPIN	Q9xd13	leptospira	628	4	8.2	74	1	WDNM_RAT	P14730	rattus norv
556	4	8.2	37	1	RL36_MYCGE	P47420	mycoplasma	629	4	8.2	74	1	YCX1_PORPU	P51336	porphyra pu
557	4	8.2	37	1	RL36_MYCLE	Q9x7a2	mycobacteri	630	4	8.2	75	1	YCX1_PORPU	P51336	porphyra pu
558	4	8.2	37	1	RL36_MYCPN	P52864	mycoplasma	631	4	8.2	76	1	RS37_YEAST	P05759	saccharomyc
559	4	8.2	37	1	RL36_MYCSP	P38015	mycoplasma	632	4	8.2	77	1	YDCE_ECOLI	P31992	escherichia
560	4	8.2	37	1	RL36_MYCTU	P45810	mycobacteri	633	4	8.2	78	1	YCX1_DICDH	P02634	rattus norv
561	4	8.2	37	1	RL36_STRCO	O86772	streptomyce	634	4	8.2	78	1	YD80_METJA	P30160	dictyeta di
562	4	8.2	37	1	RL36_SYNPE	O24707	synecococc	635	4	8.2	78	1	YD09_BPL2	P58775	methanococ
563	4	8.2	37	1	RL36_THETH	P80256	thermus aqu	636	4	8.2	79	1	NSGX_HUMAN	P42544	bacterioph
564	4	8.2	37	1	RL36_UREPA	O83239	treponema p	637	4	8.2	79	1	YIAO_BACSU	P37509	bacillus su
565	4	8.2	37	1	RL36_VIBCH	Q9pqn7	ureaplasma	638	4	8.2	81	1	PORD_METH	P56815	methanobact
566	4	8.2	37	1	RL36_VIBCH	P78001	vibriol chol	639	4	8.2	82	1	RBS_SINAL	P13951	sinapis alb
567	4	8.2	37	1	SKK2_LEIQH	P45628	leirus qui	640	4	8.2	82	1	Y056_NPVOP	O10314	orgyia pseu
568	4	8.2	37	1	RL36_BUCAI	P57570	buchnera ap	641	4	8.2	82	1	YKD3_CAEEL	Q03561	caenorhabdi
569	4	8.2	38	1	RL36_ECOLI	P21194	escherichia	642	4	8.2	83	1	CNCG_BOVIN	P22571	bos taurus
570	4	8.2	38	1	RL36_LACIA	P27146	lactococcus	643	4	8.2	83	1	CNCG_HUMAN	P13956	homo sapien
571	4	8.2	38	1	RL36_SYNV3	P73300	synecocyst	644	4	8.2	83	1	CNCG_SPETR	O55175	spermophilu
572	4	8.2	39	1	AMP1_CHICK	P80389	gallus gall	645	4	8.2	84	1	YBFJ_ECOLI	P46146	escherichia
573	4	8.2	39	1	GLI2_CHICK	P46157	gallus gall	646	4	8.2	84	1	YS14_CAEEL	Q09362	caenorhabdi
574	4	8.2	40	1	UPKB_MOUSE	Q922c6	mus musculu	647	4	8.2	86	1	NI2B_PEA	Q00665	pisum sativ
575	4	8.2	43	1	NT3_RAJCL	P25434	raya clavat	648	4	8.2	86	1	SELW_SHEEP	O19097	ovis aries
576	4	8.2	43	1	PSBN_CYPAP	P48108	cyanophora	649	4	8.2	86	1	YIDD_PROMI	P22834	proteus mlr
577	4	8.2	44	1	DERM_PIG	P45846	sus scrofa	650	4	8.2	87	1	CNRG_BOVIN	Q04972	bos taurus
578	4	8.2	44	1	MF22_SCHPO	P34069	schizosacch	651	4	8.2	87	1	CNRG_CANFA	P54827	canis famli
579	4	8.2	44	1	PSBN_CHLRE	Q06480	chlamydomon	652	4	8.2	87	1	CNRG_HUMAN	P18545	homo sapien
580	4	8.2	44	1	PSBN_NEPOL	Q9tkw6	nephroselmi	653	4	8.2	87	1	CNRG_MOUSE	P09174	mus musculu
581	4	8.2	45	1	RL36_CHLPN	Q926x0	chlamydia p	654	4	8.2	87	1	RR15_TOBAC	P06373	nicotiana t
582	4	8.2	45	1	RL36_CHLTR	O84791	chlamydia t	655	4	8.2	89	1	DYLL_HUMAN	Q9y3p0	homo sapien
583	4	8.2	45	1	RS22_ECOLI	P28690	escherichia	656	4	8.2	89	1	NEUY_MOUSE	P57774	mus musculu
584	4	8.2	46	1	AX1_BETVU	P81493	beta vulgar	657	4	8.2	89	1	RL34_METJA	P54053	methanococ
585	4	8.2	46	1	GCHI_BACPU	P48063	bacillus pu	658	4	8.2	89	1	SV18_HUMAN	P55774	h small ind
586	4	8.2	49	1	DISI_ECHCA	P17347	echis carin	659	4	8.2	90	1	DBH_BACST	P02346	bacillus st
587	4	8.2	49	1	Y3K8_SSVI	P20204	suifolobus	660	4	8.2	90	1	DBH_THEMEA	P02346	thermotoga
588	4	8.2	49	1	YBHT_ECOLI	P75759	escherichia	661	4	8.2	90	1	HBAL_UROHA	P18979	uromastix h
589	4	8.2	50	1	ITH2_BOVIN	P56651	bos taurus	662	4	8.2	90	1	NOLS_RHIME	Q52975	rhizobium m
590	4	8.2	50	1	YACG_ECOLI	P36681	escherichia	663	4	8.2	90	1	RS15_CAMJE	P49392	campylobact
591	4	8.2	51	1	INS_ACOCA	P01324	acomys cahi	664	4	8.2	91	1	ACCD_ANTFO	Q31796	anthoceros
592	4	8.2	51	1	INS_ANGRO	P42633	anguilla ro	665	4	8.2	91	1	Y909_METJA	Q58319	methanococc
593	4	8.2	51	1	INS_BALPH	P01312	balaeonopter	666	4	8.2	92	1	ARN_BPT4	P39510	bacterioph
594	4	8.2	51	1	INS_DIDMA	P18109	didelphis m	667	4	8.2	92	1	CAL_CANFA	P41547	canis famli
595	4	8.2	52	1	INS_PTAME	P81881	piaractus m	668	4	8.2	92	1	DBH_BACSU	P08821	bacillus su
596	4	8.2	52	1	RUBR_MEGEL	P00271	megasphaera	669	4	8.2	92	1	IM13_DROME	Q9vtn3	drosophila
597	4	8.2	54	1	APR_HUMAN	Q13794	homo sapien	670	4	8.2	92	1	YLC1_YEREN	P16161	yersinia en
598	4	8.2	55	1	ATP8_ANAPL	P50655	anas platyr	671	4	8.2	93	1	E311_ADE05	P17590	human adeno
599	4	8.2	55	1	ATP8_LOXNO	Q9mdj1	loxigilla n	672	4	8.2	93	1	HMEN_SCHAM	P14150	schistocerc
600	4	8.2	55	1	ATP8_SQAC	Q9z250	squalus aca	673	4	8.2	93	1	IFHB_BUCAP	Q44654	buchnera ap
601	4	8.2	55	1	ATP8_XENIA	P03931	xenopus lae	674	4	8.2	93	1	NI2A_MEDSA	Q40361	medicago sa
602	4	8.2	55	1	ISH1_STOHE	P31713	stoichactis	675	4	8.2	93	1	Y073_METJA	Q60379	methanococ
603	4	8.2	56	1	ANCI_APIME	P56682	apis mellif	676	4	8.2	93	1	YF83_YEAST	O14464	saccharomyc
604	4	8.2	56	1	RL32_ECOLI	P02435	escherichia	677	4	8.2	93	1	YOIC_CAEEL	Q09283	caenorhabdi
605	4	8.2	59	1	PSBK_PINTH	P41598	pinus thunb	678	4	8.2	94	1	AFP_ASPGI	P17337	aspergillus
606	4	8.2	59	1	ATP8_BPP22	P57017	bacterioph	679	4	8.2	94	1	CKS1_CAEEL	Q17868	caenorhabdi
607	4	8.2	61	1	ATP8_CHEMY	Q9xpi2	chelonoria my	680	4	8.2	94	1	DBH_HELPJ	Q92108	helicobacte
608	4	8.2	61	1	IPST_ANGAN	P11705	anguilla an	681	4	8.2	94	1	DBH_HELPJ	O25506	helicobacte
609	4	8.2	61	1	N014_PEA	P26415	pisum sativ	682	4	8.2	94	1	IFHB_ECOLI	P08756	escherichia
610	4	8.2	64	1	Y592_HAEIN	P44021	haemophilus	683	4	8.2	94	1	IFHB_ERWCH	P37983	erwinia chr
611	4	8.2	65	1	GLLI_CHICK	P46156	gallus gall	684	4	8.2	94	1	IFHB_PSEAE	Q51473	pseudomonas
612	4	8.2	65	1	YCX2_GUIFH	O78421	guillardia	685	4	8.2	94	1	IFHB_SERMA	P23303	serratia ma
613	4	8.2	66	1	SECE_RICPR	P50054	rickettsia	686	4	8.2	95	1	VP10_NPVAC	P04870	autographa
614	4	8.2	67	1	ATPE_SCHPO	P87316	schizosacch	687	4	8.2	95	1	CH10_BORPE	P48221	bordetella
615	4	8.2	67	1	DISB_ECHCA	P81631	echis carin	688	4	8.2	95	1	DBH_THETH	P19436	thermus aqu
616	4	8.2	68	1	ATOX_HUMAN	O00244	homo sapien	689	4	8.2	95	1	RL31_UREPA	Q9prel	ureaplasma
617	4	8.2	68	1	ATOX_MOUSE	O08997	mus musculu	690	4	8.2	95	1	U119_CANFA	Q19177	canis famli

691	RL4_XENTR	1	96	8.2	4	14117 xenopus tro	764	1	INS2_MOUSE	P01326 mus musculus
692	BOR_LAMBD	1	97	8.2	4	P26814 bacterioph	765	1	INS2_RAT	P01323 rattus norv
693	NEUY_CHICK	1	97	8.2	4	P28673 gallus gall	766	1	INS_CANFA	P01321 canis famill
694	NEUY_HUMAN	1	97	8.2	4	P01303 homo sapien	767	1	INS_CERAE	P30407 cercopithe
695	NEUY_XENLA	1	97	8.2	4	P33689 xenopus lae	768	1	INS_CRILO	P01313 cricetus
696	NO75_MEDSA	1	97	8.2	4	P11728 medicago sa	769	1	INS_HUMAN	P01308 homo sapien
697	RL31_MYCPN	1	97	8.2	4	P78020 mycoplasma	770	1	INS_MACFA	P30406 macaca fasc
698	NEUY_RAT	1	98	8.2	4	P07808 rattus norv	771	1	INS_PANTR	P30410 pan troglod
699	NEUY_TORMA	1	98	8.2	4	P28674 torpedo mar	772	1	INS_RABIT	P01311 cryctologus
700	VE7_HPV58	1	98	8.2	4	P28557 human papil	773	1	INS_GANLU	P14945 ganoderma l
701	VG04_BPMD2	1	98	8.2	4	O64200 mycobacteri	774	1	L28_GANLU	P20799 pisum sativ
702	YX1J_BACSU	1	98	8.2	4	P42320 bacillus su	775	1	N12A_PEA	P77214 escherichia
703	CH10_MYCAV	1	99	8.2	4	O86017 mycobacteri	776	1	YLCC_ECOLI	O43638 homo sapien
704	CH10_MYCBO	1	99	8.2	4	P15020 mycobacteri	777	1	FREA_MOUSE	O61574 mus musculu
705	CH10_MYCLE	1	99	8.2	4	P24301 mycobacteri	778	1	FREA_MOUSE	O61574 mus musculu
706	CH10_MYCTU	1	99	8.2	4	O9621 mycobacteri	779	1	RLA3_LEITN	O06382 leishmania
707	RS20_CHLPN	1	99	8.2	4	O927f2 chlamydia p	780	1	YHO7_YEAST	P38804 saccharomyc
708	IHPB_PSEPU	1	100	8.2	4	O52285 pseudomonas	781	1	CISY_BARVB	P51035 bartonella
709	NO12_VICSA	1	100	8.2	4	O41701 vicia sativ	782	1	FER1_CAUCR	O45972 caulobacter
710	Y953_METUA	1	100	8.2	4	Q58363 methanococc	783	1	OLF8_MOUSE	O60892 trypanosoma
711	TBCA_ARATH	1	101	8.2	4	O04350 arabidopsis	784	1	RLA3_TRYCR	P26795 trypanosoma
712	MTFB_METWA	1	101	8.2	4	P80655 methanosarc	785	1	VNUN_BPHKO	P18683 bacterioph
713	VE7_PAPVD	1	102	8.2	4	P03131 deer papill	786	1	Y122_CAEEL	P39335 caenorhabdi
714	VE7_PAPVE	1	102	8.2	4	P11332 european el	787	1	Y122_CAEEL	P39335 caenorhabdi
715	Y266_BORBU	1	102	8.2	4	Q44754 borrelia bu	788	1	Y122_CAEEL	P39335 caenorhabdi
716	VE7_PAPVE	1	103	8.2	4	Q28988 sus scrofa	789	1	Y122_CAEEL	P39335 caenorhabdi
717	LAC_CHICK	1	103	8.2	4	P20763 gallus gall	790	1	Y122_CAEEL	P39335 caenorhabdi
718	NO12_MEDTR	1	103	8.2	4	P30365 medicago tr	791	1	Y122_CAEEL	P39335 caenorhabdi
719	Y440_MYCPN	1	103	8.2	4	P75074 mycoplasma	792	1	Y122_CAEEL	P39335 caenorhabdi
720	CMGA_STRCA	1	104	8.2	4	P33716 struthio ca	793	1	Y122_CAEEL	P39335 caenorhabdi
721	RN30_RANPI	1	104	8.2	4	P22069 rana pipien	794	1	Y122_CAEEL	P39335 caenorhabdi
722	SMT3_ARATH	1	104	8.2	4	P55852 arabidopsis	795	1	Y122_CAEEL	P39335 caenorhabdi
723	YMK8_YEAST	1	105	8.2	4	O03759 saccharomyc	796	1	Y122_CAEEL	P39335 caenorhabdi
724	YKDK_BACSU	1	105	8.2	4	P94500 bacillus su	797	1	Y122_CAEEL	P39335 caenorhabdi
725	FER_PSEPU	1	106	8.2	4	P00213 pseudomonas	798	1	Y122_CAEEL	P39335 caenorhabdi
726	FXD4_HUMAN	1	106	8.2	4	Q12950 homo sapien	799	1	Y122_CAEEL	P39335 caenorhabdi
727	KACB_RABIT	1	106	8.2	4	P01839 cryctolaqu	800	1	Y122_CAEEL	P39335 caenorhabdi
728	YB43_VIECH	1	106	8.2	4	Q9Ksw3 vibrio chol	801	1	Y122_CAEEL	P39335 caenorhabdi
729	YLJA_ECOLI	1	106	8.2	4	P75832 escherichia	802	1	Y122_CAEEL	P39335 caenorhabdi
730	KVID_HUMAN	1	107	8.2	4	P01596 homo sapien	803	1	Y122_CAEEL	P39335 caenorhabdi
731	YKKB_BACSU	1	107	8.2	4	P54565 bacillus su	804	1	Y122_CAEEL	P39335 caenorhabdi
732	DBH_BORAD	1	108	8.2	4	Q44625 borrelia an	805	1	Y122_CAEEL	P39335 caenorhabdi
733	DBH_BORAF	1	108	8.2	4	Q57220 borrelia an	806	1	Y122_CAEEL	P39335 caenorhabdi
734	DBH_BORBU	1	108	8.2	4	Q57220 borrelia bu	807	1	Y122_CAEEL	P39335 caenorhabdi
735	DBH_BORJA	1	108	8.2	4	Q45231 borrelia ja	808	1	Y122_CAEEL	P39335 caenorhabdi
736	INS1_MOUSE	1	108	8.2	4	P01325 mus musculu	809	1	Y122_CAEEL	P39335 caenorhabdi
737	INS_ACTTR	1	108	8.2	4	P10604 actus trivi	810	1	Y122_CAEEL	P39335 caenorhabdi
738	INS_BRARE	1	108	8.2	4	O73727 brachydanio	811	1	Y122_CAEEL	P39335 caenorhabdi
739	INS_CYPCA	1	108	8.2	4	P01335 cyprinus ca	812	1	Y122_CAEEL	P39335 caenorhabdi
740	INS_PIG	1	108	8.2	4	P01315 sus scrofa	813	1	Y122_CAEEL	P39335 caenorhabdi
741	KVIB_HUMAN	1	108	8.2	4	P01594 homo sapien	814	1	Y122_CAEEL	P39335 caenorhabdi
742	KVIC_HUMAN	1	108	8.2	4	P01595 homo sapien	815	1	Y122_CAEEL	P39335 caenorhabdi
743	KVIE_HUMAN	1	108	8.2	4	P01597 homo sapien	816	1	Y122_CAEEL	P39335 caenorhabdi
744	KVIF_HUMAN	1	108	8.2	4	P01598 homo sapien	817	1	Y122_CAEEL	P39335 caenorhabdi
745	KVIG_HUMAN	1	108	8.2	4	P01599 homo sapien	818	1	Y122_CAEEL	P39335 caenorhabdi
746	KVIH_HUMAN	1	108	8.2	4	P01600 homo sapien	819	1	Y122_CAEEL	P39335 caenorhabdi
747	KVIK_HUMAN	1	108	8.2	4	P01603 homo sapien	820	1	Y122_CAEEL	P39335 caenorhabdi
748	KVIN_HUMAN	1	108	8.2	4	P01606 homo sapien	821	1	Y122_CAEEL	P39335 caenorhabdi
749	KVIP_HUMAN	1	108	8.2	4	P01608 homo sapien	822	1	Y122_CAEEL	P39335 caenorhabdi
750	KVIO_HUMAN	1	108	8.2	4	P01609 homo sapien	823	1	Y122_CAEEL	P39335 caenorhabdi
751	KVIV_HUMAN	1	108	8.2	4	P04430 homo sapien	824	1	Y122_CAEEL	P39335 caenorhabdi
752	KV5Q_MOUSE	1	108	8.2	4	P01650 mus musculu	825	1	Y122_CAEEL	P39335 caenorhabdi
753	KV5R_MOUSE	1	108	8.2	4	P01651 mus musculu	826	1	Y122_CAEEL	P39335 caenorhabdi
754	KV5S_MOUSE	1	108	8.2	4	P01652 mus musculu	827	1	Y122_CAEEL	P39335 caenorhabdi
755	KV5T_MOUSE	1	108	8.2	4	P01653 mus musculu	828	1	Y122_CAEEL	P39335 caenorhabdi
756	PT05_STYPL	1	108	8.2	4	P28197 styela plic	829	1	Y122_CAEEL	P39335 caenorhabdi
757	YC50_CYPAP	1	108	8.2	4	P48326 cyanophora	830	1	Y122_CAEEL	P39335 caenorhabdi
758	KV01_RAT	1	109	8.2	4	P01681 rattus norv	831	1	Y122_CAEEL	P39335 caenorhabdi
759	KVIT_HUMAN	1	109	8.2	4	P01612 homo sapien	832	1	Y122_CAEEL	P39335 caenorhabdi
760	VNST_BUNGE	1	109	8.2	4	P16992 bunyavirus	833	1	Y122_CAEEL	P39335 caenorhabdi
761	GLR2_SCHPO	1	110	8.2	4	Q9U12 schizosacch	834	1	Y122_CAEEL	P39335 caenorhabdi
762	HDEA_ECOLI	1	110	8.2	4	P26604 escherichia	835	1	Y122_CAEEL	P39335 caenorhabdi
763	INS1_RAT	1	110	8.2	4	P01322 rattus norv	836	1	Y122_CAEEL	P39335 caenorhabdi

837	4	8.2	121	1	HESB_PLEBO	P46053 plectonema	910	4	8.2	135	1	ANFC_SQUAC	P41319 squalus aca
838	4	8.2	121	1	MP70_MYCKA	Q49614 mycobacteri	911	4	8.2	135	1	EBSP_APUP	Q33629 apus apus (
839	4	8.2	121	1	UBCC_ATH	P56617 arbidopsi	912	4	8.2	135	1	EBSP_ENTFA	P36921 enterococcu
840	4	8.2	122	1	H2B_ATH	P40283 arbidopsi	913	4	8.2	135	1	FKB2_YEAT	P32472 saccharomyc
841	4	8.2	122	1	Y2B_METJA	P81305 methanococc	914	4	8.2	135	1	FKB2_ATH	P56793 arbidopsi
842	4	8.2	123	1	HEB1_ANAVA	P46051 anabena va	915	4	8.2	135	1	RR16_EUGR	P21512 euglena gra
843	4	8.2	123	1	HEB2_ANAVA	P46052 anabena va	916	4	8.2	135	1	RR16_HUMAN	P08526 homo sapien
844	4	8.2	123	1	Y052_NPVAC	P41456 autographa	917	4	8.2	135	1	RS9_ARCFU	Q29136 archaeoglob
845	4	8.2	123	1	YB44_YEAT	P38305 saccharomyc	918	4	8.2	135	1	YM33_MYCTU	Q10516 mycobacteri
846	4	8.2	123	1	Y002_CABEL	P34634 caenorhabdi	919	4	8.2	136	1	CAL0_MOUSE	P70160 mus musculu
847	4	8.2	124	1	CB21_RAPSA	P14584 raphanus sa	920	4	8.2	136	1	CAL0_RAT	P01257 rattus norv
848	4	8.2	124	1	HV1D_HUMAN	P01760 homo sapien	921	4	8.2	136	1	CAL1_ONCKE	P01263 oncorhynch
849	4	8.2	124	1	HV1E_HUMAN	P01761 homo sapien	922	4	8.2	136	1	R27A_SCHPO	O14388 schizosacch
850	4	8.2	124	1	RL17_MYCPN	Q59547 mycoplasma	923	4	8.2	136	1	R27B_SCHPO	O14388 schizosacch
851	4	8.2	124	1	SPOF_BACSU	P06628 bacillus su	924	4	8.2	136	1	RL27_CAEEL	P791914 caenorhabdi
852	4	8.2	124	1	VG04_VACCV	P21025 vaccinia vi	925	4	8.2	137	1	5H4_PIG	Q29006 sus scrofa
853	4	8.2	124	1	VG04_VARY	P32994 variola vir	926	4	8.2	137	1	H2B4_MAIZE	P49120 zea mays (m
854	4	8.2	124	1	YLS1_CABEL	P34386 caenorhabdi	927	4	8.2	137	1	LSM4_MOUSE	Q9qxa5 mus musculu
855	4	8.2	125	1	CALR_CHICK	P10286 gallus gall	928	4	8.2	137	1	MP12_LYNST	P25289 lymanaea sta
856	4	8.2	125	1	HV1F_HUMAN	P06336 homo sapien	929	4	8.2	137	1	RR16_VIGUN	P42353 vigina ungui
857	4	8.2	125	1	RL7_LIBAF	P41189 liberobacte	930	4	8.2	137	1	RR9_CHLVU	P56358 chlorella v
858	4	8.2	125	1	RS17_CABEL	O01692 caenorhabdi	931	4	8.2	137	1	WAP_RAT	P01174 rattus norv
859	4	8.2	125	1	RS6_HAEIN	P44375 haemophilus	932	4	8.2	138	1	CAL_CHICK	P07660 gallus gall
860	4	8.2	125	1	Y394_RICPR	Q92dd7 rickettsia	933	4	8.2	138	1	DSBH_BACSU	Q32217 bacillus su
861	4	8.2	126	1	CD59_RAT	P27274 rattus norv	934	4	8.2	138	1	GCSH_PYRAB	Q9v0g1 pyrococcus
862	4	8.2	126	1	NG24_MOUSE	Q92lq4 mus musculu	935	4	8.2	138	1	GTH2_CLAGA	P53543 clarias gar
863	4	8.2	126	1	WNT1_EUMSK	P28113 eumeces ski	936	4	8.2	138	1	HEX9_ADE07	P03283 human adeno
864	4	8.2	126	1	WNT1_PITME	P28139 pituophis m	937	4	8.2	138	1	ID5A_ADEPA	P09941 adenanthera
865	4	8.2	126	1	WNT1_SCHOC	P28141 sceloporos	938	4	8.2	138	1	PT56_SACKL	Q02997 saccharomyc
866	4	8.2	126	1	YAWE_SCHPO	Q10188 schizosacch	939	4	8.2	138	1	VIVA_BPT7	P03723 bacterioph
867	4	8.2	127	1	CAL2_HUMAN	P10092 homo sapien	940	4	8.2	138	1	X_HPBG5	Q03168 ground squi
868	4	8.2	127	1	HOL2_HOLDI	Q25054 holotrichia	941	4	8.2	138	1	Y178_RICPR	Q92dv5 rickettsia
869	4	8.2	127	1	YF51_HELPY	O26075 helicobacte	942	4	8.2	139	1	LSM4_HUMAN	Q9y4z0 homo sapien
870	4	8.2	128	1	CAL1_HUMAN	P06881 homo sapien	943	4	8.2	139	1	YNSB_ECOLI	P04381 escherichia
871	4	8.2	128	1	CAL1_RAT	P01256 rattus norv	944	4	8.2	139	1	YNSB_ECOLI	P04381 escherichia
872	4	8.2	128	1	HSL0_SALTY	O30911 salmonella	945	4	8.2	140	1	YNSB_ECOLI	P04381 escherichia
873	4	8.2	128	1	IF5A_ARCFU	O29612 archaeoglob	946	4	8.2	140	1	CSF2_CAVPO	Q50481 cavia porce
874	4	8.2	128	1	KV5E_MOUSE	P01637 mus musculu	947	4	8.2	140	1	GTH2_ANGAN	P27767 angulla an
875	4	8.2	128	1	VL05_VACCV	P07615 vaccinia vi	948	4	8.2	140	1	YNU5_YEAT	P40162 saccharomyc
876	4	8.2	128	1	VL05_VARY	P33043 variola vir	949	4	8.2	140	1	YQIB_ECOLI	P36652 escherichia
877	4	8.2	129	1	CARP_MOUSE	P56388 mus musculu	950	4	8.2	141	1	YQ06_METJA	O60305 methanococ
878	4	8.2	129	1	CARP_RAT	P49192 rattus norv	951	4	8.2	141	1	ARSC_YEREN	P74984 yersinia en
879	4	8.2	129	1	KV1X_HUMAN	P04431 homo sapien	952	4	8.2	141	1	CAL0_HUMAN	P01258 homo sapien
880	4	8.2	129	1	KV1X_HUMAN	P04432 homo sapien	953	4	8.2	141	1	CSF2_MOUSE	P01587 mus musculu
881	4	8.2	129	1	RL7_TREPA	O83268 treponema p	954	4	8.2	141	1	VTU1_DROME	P11449 drosophila
882	4	8.2	129	1	RS17_CHICK	P08636 gallus gall	955	4	8.2	141	1	YK13_YEAT	P36128 saccharomyc
883	4	8.2	129	1	VMOR_BPMU	P23848 bacterioph	956	4	8.2	142	1	AP17_HUMAN	P53680 homo sapien
884	4	8.2	129	1	YEQ2_YEAT	P40046 saccharomyc	957	4	8.2	142	1	AP17_MOUSE	Q00380 mus musculu
885	4	8.2	129	1	YP73_GVCL	P41730 cryptophleb	958	4	8.2	142	1	RHIC_ORYRH	O76145 oryctes rhl
886	4	8.2	130	1	CW36_YEAT	P25603 saccharomyc	959	4	8.2	142	1	RLK4_SPIOL	P27684 spinacia ol
887	4	8.2	130	1	MIA_MOUSE	O61865 mus musculu	960	4	8.2	142	1	RL16_THEMA	P38509 thermotoga
888	4	8.2	130	1	MIA_RAT	O62946 rattus norv	961	4	8.2	142	1	RS6_HELPY	Q92jv1 helicobacte
889	4	8.2	130	1	Y06Q_BPT4	P39222 bacterioph	962	4	8.2	142	1	VG09_BPT1	P56013 helicobacte
890	4	8.2	130	1	YEW5_YEAT	P40082 saccharomyc	963	4	8.2	142	1	YIC9_YEAT	P40538 saccharomyc
891	4	8.2	130	1	YHFU_ECOLI	P45547 escherichia	964	4	8.2	143	1	CAL_SHEEP	P01261 ovis aries
892	4	8.2	130	1	YKL5_YEAT	P36073 saccharomyc	965	4	8.2	143	1	GCS1_AQUAE	O67151 aquifex aeo
893	4	8.2	131	1	CAIF_ECOLI	O47081 escherichia	966	4	8.2	143	1	HMGB_TETTH	P40626 tetrahymena
894	4	8.2	131	1	CHHB_BOMMO	P05688 bombyx mori	967	4	8.2	143	1	RL16_MARPO	P06383 marichantia
895	4	8.2	131	1	HSLR_HAEIN	P44754 haemophilus	968	4	8.2	144	1	BT12_BLOTA	Q17282 blomia trop
896	4	8.2	131	1	MIA_HUMAN	Q16674 homo sapien	969	4	8.2	144	1	END2_BPT4	P07059 bacterioph
897	4	8.2	132	1	ALK1_HUMAN	P03973 homo sapien	970	4	8.2	144	1	IL9_MOUSE	P15247 mus musculu
898	4	8.2	132	1	HSLR_AERSA	Q44264 aeromonas s	971	4	8.2	144	1	RL16_BACHD	Q929k7 bacillus ha
899	4	8.2	132	1	IF5A_METJA	O58625 methanococc	972	4	8.2	144	1	RL16_BACSU	P14577 bacillus su
900	4	8.2	132	1	RRF_CLOPE	Q46293 clostridium	973	4	8.2	145	1	AZUP_PARDT	P80401 paracoccus
901	4	8.2	132	1	RS8_RICPR	Q9zcr9 rickettsia	974	4	8.2	145	1	CYTF_HUMAN	O76096 homo sapien
902	4	8.2	133	1	AGSW_BOVIN	Q29414 bos taurus	975	4	8.2	145	1	H2B_CAPAN	O49118 capsicum an
903	4	8.2	133	1	CYB5_HUMAN	P00167 homo sapien	976	4	8.2	145	1	PA21_BOVIN	P00593 bos taurus
904	4	8.2	133	1	PA23_OXYSC	P00616 oxyuranus s	977	4	8.2	145	1	PK18_PEA	P11891 pisum sativ
905	4	8.2	133	1	PA2D_PSETE	P23028 pseudonaja	978	4	8.2	145	1	YGL3_SYNY3	P73841 synechocyst
906	4	8.2	134	1	CAL2_RAT	P10093 rattus norv	979	4	8.2	145	1	YPH2_MYCCA	P45614 mycoplasma
907	4	8.2	134	1	RS17_CRIGR	P06584 cricetus	980	4	8.2	146	1	H2B_TOBAC	P93354 nicotiana t
908	4	8.2	134	1	RS17_HUMAN	P08708 homo sapien	981	4	8.2	147	1	AP17_YEAT	Q00381 saccharomyc
909	4	8.2	134	1	RS17_RAT	P04644 rattus norv	982	4	8.2	147	1	H2B_GOSHI	O22582 gossypium h

983 P54357 drosophila
 984 Q55169 synechocyst
 985 P34096 homo sapien
 986 P15468 sus scrofa
 987 Q08127 anguilla an
 988 P51668 homo sapien
 989 P51669 homo sapien
 990 P47986 homo sapien
 991 P25867 drosophila
 992 P35129 caenorhabdi
 993 P43102 candida alb
 994 P46595 schizosacch
 995 P75299 mycoplasma
 996 P4397 galeorhinus
 997 P02406 saccharomyc
 998 P35135 lycopersico
 999 P15731 saccharomyc
 1000 P15732 saccharomyc

ALIGNMENTS

RESULT 1
 VGLG_HRSVA
 ID VGLG_HRSVA STANDARD; PRT; 298 AA.
 AC P03423;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).
 GN G.

OS Human respiratory syncytial virus (strain A2).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
 OX NCBI_TaxID=11259;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=85216636; PubMed=3858865;
 RA Wertz G.W., Collins P.L., Huang Y., Gruber C., Levine S., Ball L.A.;
 RT "Nucleotide sequence of the G protein gene of human respiratory
 syncytial virus reveals an unusual type of viral membrane protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:4075-4079(1985).
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=86067198; PubMed=4069997;
 RA Satake M., Coligan J.E., Elango N., Norrby E., Venkatesan S.;
 RT "Respiratory syncytial virus envelope glycoprotein (G) has a novel
 structure.";
 RL Nucleic Acids Res. 13:7795-7812(1985).
 RN [3]

RP SEQUENCE FROM N.A.
 RX MEDLINE=95266253; PubMed=7747420;
 RA Conhorts M., Crowe J.E. Jr., Firestone C.Y., Murphy B.R., Collins P.L.;
 RT "A cold-passaged, attenuated strain of human respiratory syncytial
 virus contains mutations in the F and L genes.";
 RL Virology 208:478-484(1995).
 RN [4]

RP SEQUENCE FROM N.A.
 RX MEDLINE=97187925; PubMed=9035372;
 RA Crowe J.E. Jr., Firestone C.Y., Whitehead S.S., Collins P.L.,
 RA Murphy B.R.;
 RT "Acquisition of the ts phenotype by a chemically mutagenized cold-
 passaged human respiratory syncytial virus vaccine candidate results
 from the acquisition of a single mutation in the polymerase (L)
 gene.";
 RL Virus Genes 13:269-273(1996).

CC -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
 RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
 HEMAGGLUTININATING ACTIVITIES.
 CC -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
 CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
 CC -1- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS

CC DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
 CC
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EMBL; M11486; AAB59857.1; -
 EMBL; X03149; CAA26928.1; -
 EMBL; U50362; AAB86663.1; -
 EMBL; U50363; AAB86675.1; -
 EMBL; U63644; AAC55969.1; -
 PIR; A04039; MGNZ.
 DR InterPro: IPR000925; -
 DR Pfam: PF00802; Glycoprotein_G; 1.
 DR Transmembrane: Glycoprotein.

KW DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 38 66
 FT DOMAIN 67 298 EXTRACELLULAR (POTENTIAL).
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 298 AA; 32586 MW; 993C3D2D68BC634 CRC64;

Query Match 100.0%; Score 49; DB 1; Length 298;
 Best Local Similarity 100.0%; Pred. No. 3,7e-45;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KORQKPPSKPNDFEFVPCISCSNPTCAICKRIPNKKPGKK 49
 Db 149 KORQKPPSKPNDFEFVPCISCSNPTCAICKRIPNKKPGKK 197

RESULT 2
 VGLG_HRSV2

ID VGLG_HRSV2 STANDARD; PRT; 297 AA.
 AC P27021;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-AUG-1992 (Rel. 23, Last annotation update)
 DE MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).
 GN G.
 OS Human respiratory syncytial virus (strain rsb642).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
 OX NCBI_TaxID=11252;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91374005; PubMed=1895054;
 RA Cane P.A., Matthews D.A., Pringle C.R.;
 RT "Identification of variable domains of the attachment (G) protein of
 subgroup A respiratory syncytial viruses.";
 RL J. Gen. Virol. 72:2091-2096(1991).
 CC -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
 RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
 HEMAGGLUTININATING ACTIVITIES.
 CC -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
 CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
 CC -1- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
 DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
 CC
 CC PIR; JQ1204; JQ1204.
 DR InterPro: IPR000925; -
 DR Pfam: PF00802; Glycoprotein_G; 1.
 DR Transmembrane: Glycoprotein.
 FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 38 66
 FT DOMAIN 67 297 EXTRACELLULAR (POTENTIAL).
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 297 AA; 32745 MW; FC72A7F3A8EBF67C CRC64;

Query Match 98.0%; Score 48; DB 1; Length 297;
Best Local Similarity 100.0%; Pred. No. 4.3e-44;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNDFEVEFVPCISCSNNPTCWAICKRIPNKKPGK 48
|||||
DB 149 KORQKPPSKPNDFEVEFVPCISCSNNPTCWAICKRIPNKKPGK 196

RESULT 3

VGLG_HRSV3
ID VGLG_HRSV3 STANDARD; PRT; 297 AA.
AC P27022;

DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).

GN G.
OS Human respiratory syncytial virus (strain rsb1734).

OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.

OX NCBI_TaxID=11253;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91374005; PubMed=1895054;

RA Cane P.A., Matthews D.A., Pringle C.R.;

RT "Identification of variable domains of the attachment (G) protein of
subgroup A respiratory syncytial viruses.";

RL J. Gen. Virol. 72:2091-2096(1991).

CC -!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
HEMAGGLUTININATING ACTIVITIES.

CC -!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.

CC -!- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.

DR PIR: JQ1205; JQ1205.

DR InterPro: IPR000925; -.

DR Pfam: PF00802; Glycoprotein_G; 1.

KW Transmembrane; Glycoprotein.

FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 38 66 POTENTIAL.

FT DOMAIN 67 297 EXTRACELLULAR (POTENTIAL).

FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 297 AA; 32525 MW; 48448F9E091E1802 CRC64;

Query Match 98.0%; Score 48; DB 1; Length 297;
Best Local Similarity 100.0%; Pred. No. 4.3e-44;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNDFEVEFVPCISCSNNPTCWAICKRIPNKKPGK 48
|||||
DB 149 KORQKPPSKPNDFEVEFVPCISCSNNPTCWAICKRIPNKKPGK 196

RESULT 4

VGLG_HRSV4

ID VGLG_HRSV4 STANDARD; PRT; 297 AA.

AC P27023;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 01-AUG-1992 (Rel. 23, Last annotation update)

DE MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).

GN G.

OS Human respiratory syncytial virus (strain rsb5857).

OC Viruses; ssRNA negative-strand viruses; Mononegavirales;

OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11254;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91374005; PubMed=1895054;

RA Cane P.A., Matthews D.A., Pringle C.R.;

RT "Identification of variable domains of the attachment (G) protein of
subgroup A respiratory syncytial viruses.";

RL J. Gen. Virol. 72:2091-2096(1991).

CC -!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
HEMAGGLUTININATING ACTIVITIES.

CC -!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.

CC -!- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.

DR PIR: JQ1206; JQ1206.

DR InterPro: IPR000925; -.

DR Pfam: PF00802; Glycoprotein_G; 1.

KW Transmembrane; Glycoprotein.

FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 38 66 POTENTIAL.

FT DOMAIN 67 297 EXTRACELLULAR (POTENTIAL).

FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 297 AA; 32772 MW; 10488CCA47596BE CRC64;

Query Match 81.6%; Score 40; DB 1; Length 297;

Best Local Similarity 100.0%; Pred. No. 1.4e-35;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KPNDHFEEVFNFCISCSNNPTCWAICKRIPNKKPGK 49
|||||

DB 158 KPNDHFEEVFNFCISCSNNPTCWAICKRIPNKKPGK 197

RESULT 5

VGLG_HRSV6

ID VGLG_HRSV6 STANDARD; PRT; 297 AA.

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 01-AUG-1992 (Rel. 23, Last annotation update)

DE MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).

GN G.

OS Human respiratory syncytial virus (strain rsb6256).

OC Viruses; ssRNA negative-strand viruses; Mononegavirales;

OC Paramyxoviridae; Pneumovirinae; Pneumovirus.

OX NCBI_TaxID=11256;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91374005; PubMed=1895054;

RA Cane P.A., Matthews D.A., Pringle C.R.;

RT "Identification of variable domains of the attachment (G) protein of
subgroup A respiratory syncytial viruses.";

RL J. Gen. Virol. 72:2091-2096(1991).

CC -!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
HEMAGGLUTININATING ACTIVITIES.

CC -!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.

CC -!- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.

DR PIR: JQ1208; JQ1208.

DR InterPro: IPR000925; -.

DR Pfam: PF00802; Glycoprotein_G; 1.

KW Transmembrane; Glycoprotein.

FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).

TRANSMEM	38	66	CATIONIC (POTENTIAL).
DOMAIN	67	298	POTENTIAL.
CARBOHYD	103	103	EXTRACELLULAR (POTENTIAL).
CARBOHYD	135	135	N-LINKED (GLCNAC.) (POTENTIAL).
CARBOHYD	237	237	N-LINKED (GLCNAC.) (POTENTIAL).
CARBOHYD	250	250	N-LINKED (GLCNAC.) (POTENTIAL).
CARBOHYD	251	251	N-LINKED (GLCNAC.) (POTENTIAL).
CARBOHYD	294	294	N-LINKED (GLCNAC.) (POTENTIAL).
SEQUENCE	298 AA	32781 MW	B79FEFA4BA47B0E CRC664.

RESULT	8			
VGLG_HRSV5				
ID	VGLG_HRSV5	STANDARD;	PRT;	298 AA.
AC	P27024;			
DT	01-AUG-1992	(Rel. 23, Created)		
DT	01-AUG-1992	(Rel. 23, Last sequence update)		
DT	30-MAY-2000	(Rel. 39, Last annotation update)		
DE	MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).			
GN	G.			
OS	Human respiratory syncytial virus (strain rsb6190).			
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales;			
OC	Paramyxoviridae; Pneumovirinae; Pneumovirus.			
OX	NCBI TaxId=11255;			

```

RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=91374005; PubMed=1895054;
RA  Cane P.A., Matthews D.A., Pringle C.R.;
RT  "Identification of variable domains of the attachment (G) protein of
RL  subgroup A respiratory syncytial viruses.";
RL  J. Gen. Virol. 72:2091-2096(1991).
CC  -!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
CC  RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
CC  HEMAGGLUTININATING ACTIVITIES.
CC  -!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
CC  CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
CC  -!- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
CC  DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
CC  PIR: JQ1207; JQ1207.
DR  InterPro: IPR000925; -.
DR  Pfam: PF00802; Glycoprotein_G; 1.
KW  Transmembrane; Glycoprotein.
FT  DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM 38 66 POTENTIAL.
FT  DOMAIN 67 298 EXTRACELLULAR (POTENTIAL).
FT  CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 250 250 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ  SEQUENCE 298 AA; 32769 MW; 4D74B854D34D7BA5 CRC64;

Query Match 67.3%; Score 33; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 3.9e-28;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  10 KPNDPFHEVFNFPVCSICNNPTCWAICKRIP 42
Db  158 KPNDPFHEVFNFPVCSICNNPTCWAICKRIP 190
|||||
|||||

RESULT 9
VGLG_HRSV1
ID  VGLG_HRSV1 STANDARD; PRT; 292 AA.
AC  P20896;
DT  01-FEB-1991 (Rel. 17, Created)
DT  01-FEB-1991 (Rel. 17, Last sequence update)
DT  01-NOV-1991 (Rel. 20, Last annotation update)
DE  MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).
GN  G.
OS  Human respiratory syncytial virus (subgroup B / strain 18537).
OC  Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC  Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX  NCBI_TaxID=11251;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=87289657; PubMed=2441388;
RA  Johnson P.R., Spriggs M.K., Olmsted R.A., Collins P.L.;
RT  "The G glycoprotein of human respiratory syncytial viruses of
RT  subgroups A and B: extensive sequence divergence between
RT  antigenically related proteins.";
RL  Proc. Natl. Acad. Sci. U.S.A. 84:5625-5629(1987).
CC  -!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
CC  RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
CC  HEMAGGLUTININATING ACTIVITIES.
CC  -!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
CC  CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
CC  -!- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
CC  DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
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CC  EMBL; M17213; AAA47412.1; -.
DR  PIR: B32703; MGNZ18.
DR  InterPro: IPR000925; -.
DR  Pfam: PF00802; Glycoprotein_G; 1.
KW  Transmembrane; Glycoprotein.
FT  DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM 38 66 POTENTIAL.
FT  DOMAIN 67 292 EXTRACELLULAR (POTENTIAL).
FT  CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ  SEQUENCE 292 AA; 32306 MW; BC8C59F69CA7AFC2 CRC64;

Query Match 26.5%; Score 13; DB 1; Length 292;
Best Local Similarity 100.0%; Pred. No. 7e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  16 HFEVFNFPVCSIC 28
Db  164 HFEVFNFPVCSIC 176
|||||
|||||

RESULT 10
VGLG_HRSV8
ID  VGLG_HRSV8 STANDARD; PRT; 292 AA.
AC  P23041;
DT  01-NOV-1991 (Rel. 20, Created)
DT  01-NOV-1991 (Rel. 20, Last sequence update)
DT  01-AUG-1992 (Rel. 23, Last annotation update)
DE  MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).
GN  G.
OS  Human respiratory syncytial virus (subgroup B / strain 8/60).
OC  Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC  Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX  NCBI_TaxID=11258;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=90357765; PubMed=1697126;
RA  Sullender W.M., Anderson K., Wertz G.W.;
RT  "The respiratory syncytial virus subgroup B attachment glycoprotein:
RT  analysis of sequence, expression from a recombinant vector, and
RT  evaluation as an immunogen against homologous and heterologous
RT  subgroup virus challenge.";
RL  Virology 178:195-203(1990).
RN  [2]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=91374595; PubMed=1895391;
RA  Sullender W.M., Mufson M.M., Anderson L.J., Wertz G.W.;
RT  "Genetic diversity of the attachment protein of subgroup B
RT  respiratory syncytial viruses.";
RL  J. Virol. 65:5425-5434(1991).
CC  -!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
CC  RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
CC  HEMAGGLUTININATING ACTIVITIES.
CC  -!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
CC  CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
CC  -!- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
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CC  EMBL; M55633; AAA47413.1; -.
DR  EMBL; M73545; AAA47408.1; -.
DR  PIR: A37077; MGNZ60.

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DR InterPro: IPR000925; -
DR Pfam: PF00802; Glycoprotein_G; 1.
KW Transmembrane; Glycoprotein.
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 38 66
FT DOMAIN 67 292
FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 292 AA; 32143 MW; 8EC60C85EF057BB5 CRC64;

Query Match 26.5%; Score 13; DB 1; Length 292;
Best Local Similarity 100.0%; Pred. No. 7e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 HFEVFNFPVCSIC 28
DB 164 HFEVFNFPVCSIC 176

RESULT 11
POLSEEVVP
ID POLSEEVVP STANDARD; PRT; 1255 AA.
AC P36332;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE STRUCTURAL POLYPEPTIDE [CONTAINS: COAT PROTEIN C (EC 3.4.21.-); SPIKE
DE GLYCOPROTEINS E3, E2 AND E1; 6 KDA PEPTIDE].
OS Venezuelan equine encephalitis virus (strain P676).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
OC Alphavirus.
OX NCBI_TaxID=36385;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93079859; PubMed=1448915;
RA Kinney R.M., Tsuchiya K.R., Snider J.M., Trent D.W.;
RT "Genetic evidence that epizootic Venezuelan equine encephalitis (VEE)
RT viruses may have evolved from enzootic VEE subtype I-D virus.";
RL Virology 191:569-580(1992).
CC -1- FUNCTION: THE CAPSID PROTEIN IS AN AUTO-PROTEASE.
CC -1- PTM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC -1- MISCELLANEOUS: THE 6 KDA POLYPEPTIDE PROBABLY SERVES AS THE SIGNAL
CC | SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN E1, WHICH IS THE VIRAL
CC | HEMAGGLUTININ.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S3.

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DR EMBL; L04653; AAC19319.1; -
DR PIR; B44213; B44213.
DR HSP; P03315; 1VCO.
DR MEROPS; S03.001.
DR InterPro: IPR000930; -
DR InterPro: IPR000936; -
DR InterPro: IPR001836; -
DR InterPro: IPR002533; -
DR InterPro: IPR002548; -
DR Pfam; PF01589; Alpha_E1_glycop; 1.
DR Pfam; PF00943; Alpha_E2_glycop; 1.
DR Pfam; PF01563; Alpha_E3_glycop; 1.
DR Pfam; PF00944; Alpha_core; 1.
DR PRINTS; PR00798; TOGAVIRIN.
KW Coat protein; Polyprotein; Transmembrane; Glycoprotein; Hydrolase;
KW Serine protease.
FT CHAIN 1 275 COAT PROTEIN C (CAPSID PROTEIN C).

FT CHAIN 276 334 SPIKE GLYCOPROTEIN E3.
FT CHAIN 335 757 SPIKE GLYCOPROTEIN E2.
FT CHAIN 758 813 6 KDA PEPTIDE.
FT CHAIN 814 1255 SPIKE GLYCOPROTEIN E1.
FT ACT_SITE 152 152 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 158 158 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 226 226 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT TRANSMEM 702 722 POTENTIAL.
FT TRANSMEM 795 814 POTENTIAL.
FT TRANSMEM 1232 1249 POTENTIAL.
FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 652 652 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 947 947 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1255 AA; 138213 MW; 33CD302F5CAE8646 CRC64;

Query Match 14.3%; Score 7; DB 1; Length 1255;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 PNKPKGK 48
DB 108 PNKPKGK 114

RESULT 12
RS13_STRCO
ID RS13_STRCO STANDARD; PRT; 126 AA.
AC O86773;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 30S RIBOSOMAL PROTEIN S13.
GN RPSM OR SC6G4.05.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Saunders D., Harris D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INVOLVED IN THE BINDING OF FMET-TRNA AND, HENCE, IN THE
CC | INITIATION OF TRANSLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE S13P FAMILY OF RIBOSOMAL PROTEINS.

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DR EMBL; AL031317; CAA20383.1; -
DR InterPro: IPR001892; -
DR Pfam; PF00416; Ribosomal_S13; 1.
DR PROSITE; PS00646; RIBOSOMAL_S13; 1.
KW Ribosomal protein.
SQ SEQUENCE 126 AA; 14219 MW; F1E92BB01DE4906F CRC64;

Query Match 12.2%; Score 6; DB 1; Length 126;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 KPGKK 49
DB 121 KPGKK 126


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RESULT 13
ID Y021_CAEEEL STANDARD; PRT; 159 AA.
AC P34671;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 01-JUN-1994 (Rel. 29, Last annotation update)
DE HYPOTHETICAL 18.0 KDA PROTEIN ZK688.1 IN CHROMOSOME III.
GN ZK688.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fraser A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
RA Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Watson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
FT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
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CC -----
DR EMBL; L16621; AAA28226.1; -.
DR PIR; S44915; S44915.
DR WormPep; ZK688.1; CE00459.
DR Hypothetical protein.
KW SEQUENCE 159 AA; 18018 MW; 74280FC07F7FF633 CRC64;
SQ SEQUENCE 159 AA; 18018 MW; 74280FC07F7FF633 CRC64;

Query Match 12.2%; Score 6; DB 1; Length 159;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PSKPNH 13
Db 44 PSKPNH 49
|||||

RESULT 14
ID RAC3_HUMAN STANDARD; PRT; 192 AA.
AC O14658;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 3 (P21-RAC3).
GN RAC3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97400509; PubMed=9252344;
RA Haataja L., Groffen J., Heisterkamp N.;
```

```
RT "Characterization of RAC3, a novel member of the Rho family.";
RL J. Biol. Chem. 272:20384-20388(1997).
CC -!- FUNCTION: MAY PLAY A ROLE IN INTRACELLULAR SIGNALING.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC; MEMBRANE-ASSOCIATED WHEN
CC ACTIVATED (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: HIGHEST LEVELS IN BRAIN, ALSO DETECTED IN
CC HEART, PLACENTA, AND PANCREAS.
CC -!- INDUCTION: EXPRESSION DOWN-REGULATED IN QUIESCENT FIBROBLASTS AND
CC CLEARLY INDUCED BY SERUM STIMULATION.
CC -!- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RHO FAMILY.
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CC -----
DR EMBL; AF008591; AAC51667.1; -.
DR HSSP; P15154; 1MH1.
DR MIM; 602050;
DR InterPro; IPR001806;
DR InterPro; IPR002380;
DR Pfam; PF00071; ras; 1.
DR PRINTS; PR00449; RASTRNSFRMG.
DR GTP-binding; Prenylation; Lipoprotein.
FT NP_BIND 10 17 GTP (BY SIMILARITY).
FT NP_BIND 57 61 GTP (BY SIMILARITY).
FT NP_BIND 115 118 GTP (BY SIMILARITY).
FT DOMAIN 32 40 EFFECTOR REGION (POTENTIAL).
FT LIPID 189 189 GERANYL-GERANYL (BY SIMILARITY).
SQ SEQUENCE 192 AA; 21379 MW; 560BBC26BB7CDF4A CRC64;

Query Match 12.2%; Score 6; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 KPGKK 49
Db 183 KPGKK 188
|||||

RESULT 15
ID Y010_MYCPN STANDARD; PRT; 212 AA.
AC P75099;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE HYPOTHETICAL PROTEIN MG010 HOMOLOG (D12_ORF212).
GN MPN014 OR MPI40.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
RA Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae.";
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -!- SIMILARITY: SOME, TO DNA PRIMASES (DNAG).
CC -----
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DR EMBL: AF000016; AAB95788.1; -

DR InterPro: IPR002936; -

DR Pfam: PF01751; Toprim; 1.

KW Hypothetical protein.

SQ SEQUENCE 212 AA; 24497 MW; 24F971B162DEC2C3 CRC64;

Query Match

12.2%; Score 6; DB 1; Length 212;

Best local Similarity 100.0%; Pred. No. 15;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NKPPSK 10

(|||||)

Db 85 NKPPSK 90

Search completed: May 21, 2001, 14:19:40
Job time: 103 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 21, 2001, 14:17:52 ; Search time 19.59 Seconds
(without alignments)
293.169 Million cell updates/sec

Title: US-09-202-035-1
Perfect score: 49
Sequence: 1 KORONKPPSKPNDFHFEVF.....NNPTCWAICKRIPNKKPGKK 49

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 374700 seqs, 117207915 residues

Word size : 0

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SPREMBL15:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_unclassified:*
- 13: sp_vertebrate:*
- 14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	49	100.0	233	14	Q9YVB3 human respi
2	48	98.0	292	14	Q9YVB2 human respi
3	48	98.0	295	14	Q86356 respiratory
4	48	98.0	295	14	Q86360 respiratory
5	48	98.0	297	14	Q82066 human respi
6	48	98.0	297	14	Q82067 human respi
7	48	98.0	297	14	Q82071 human respi
8	48	98.0	297	14	Q9YVB5 human respi
9	42	85.7	297	14	Q9YVB4 human respi
10	41	83.7	297	14	Q82070 human respi
11	40	81.6	278	14	Q9G6U1 human respi
12	40	81.6	278	14	Q9G6T7 human respi
13	40	81.6	278	14	Q9G6T4 human respi
14	40	81.6	278	14	Q9G6T3 human respi
15	40	81.6	278	14	Q9G6T1 human respi
16	40	81.6	278	14	Q9G6T0 human respi
17	40	81.6	279	14	Q9G6U0 human respi
18	40	81.6	279	14	Q9G6T9 human respi
19	40	81.6	279	14	Q9G6T8 human respi

93	7	14.3	834	5	Q9V320	Q9V320 drosophila	166	6	12.2	1889	5	Q9XZS2	Q9XZS2 drosophila
94	7	14.3	1254	14	Q9YK4	Q9YK4 venezuelan	167	6	12.2	1889	5	Q9XZS1	Q9XZS1 drosophila
95	7	14.3	1468	10	Q9SVL1	Q9SVL1 arabidopsis	168	6	12.2	1889	5	Q9XZU9	Q9XZU9 drosophila
96	6	12.2	38	8	Q9MU8	Q9MU8 mesostigma	169	5	10.2	21	10	Q41181	Q41181 nicotiana t
97	6	12.2	77	6	Q02672	Q02672 alces alces	170	5	10.2	25	4	Q9R5G8	Q9R5G8 fusobacteri
98	6	12.2	94	5	Q9XUF3	Q9XUF3 caenorhabdi	171	5	10.2	40	4	Q16128	Q16128 homo sapien
99	6	12.2	109	14	Q9IUOC8	Q9IUOC8 human respi	172	5	10.2	49	2	Q9JVE5	Q9JVE5 neisseria m
100	6	12.2	111	4	Q9NQ12	Q9NQ12 homo sapien	173	5	10.2	61	2	O50758	O50758 borrelia bu
101	6	12.2	190	2	Q53760	Q53760 staphylococ	174	5	10.2	65	2	P73358	P73358 synechocyst
102	6	12.2	191	13	Q91874	Q91874 xenopus lae	175	5	10.2	65	10	Q9MGQ5	Q9MGQ5 medicago tr
103	6	12.2	192	13	Q93466	Q93466 gallus gall	176	5	10.2	70	4	Q9PIN2	Q9PIN2 homo sapien
104	6	12.2	196	10	Q40386	Q40386 nicotiana a	177	5	10.2	70	8	Q9ZYE1	Q9ZYE1 hippotragus
105	6	12.2	196	10	Q40386	Q40386 nicotiana a	178	5	10.2	70	8	Q9ZYE0	Q9ZYE0 hippotragus
106	6	12.2	205	5	Q18977	Q18977 caenorhabdi	179	5	10.2	70	8	Q9ZXD9	Q9ZXD9 hippotragus
107	6	12.2	206	1	Q59116	Q59116 pyrococcus	180	5	10.2	70	8	Q9ZXS1	Q9ZXS1 hippotragus
108	6	12.2	218	10	Q40381	Q40381 nicotiana a	181	5	10.2	70	8	Q9ZXR9	Q9ZXR9 hippotragus
109	6	12.2	243	10	Q9SYN7	Q9SYN7 arabidopsis	182	5	10.2	70	8	Q9ZXR8	Q9ZXR8 hippotragus
110	6	12.2	244	14	Q67697	Q67697 garlic viru	183	5	10.2	70	8	Q9ZXR7	Q9ZXR7 hippotragus
111	6	12.2	299	2	O87489	O87489 pseudomonas	184	5	10.2	70	8	Q9ZXR6	Q9ZXR6 hippotragus
112	6	12.2	317	5	O44889	O44889 caenorhabdi	185	5	10.2	70	8	Q9ZXR5	Q9ZXR5 hippotragus
113	6	12.2	359	10	O23655	O23655 arabidopsis	186	5	10.2	70	8	Q9ZXR4	Q9ZXR4 hippotragus
114	6	12.2	363	3	Q99326	Q99326 saccharomyc	187	5	10.2	76	8	Q34361	Q34361 damalisus
115	6	12.2	411	10	Q9SSG7	Q9SSG7 arabidopsis	188	5	10.2	78	9	Q37833	Q37833 bacterioph
116	6	12.2	415	10	Q9SLF16	Q9SLF16 arabidopsis	189	5	10.2	83	3	Q9U027	Q9U027 schistosacch
117	6	12.2	416	10	Q9SLK0	Q9SLK0 arabidopsis	190	5	10.2	84	2	Q9JXY3	Q9JXY3 neisseria m
118	6	12.2	418	2	O54651	O54651 streptococc	191	5	10.2	87	10	O42237	O42237 arabidopsis
119	6	12.2	418	3	Q9Y7V6	Q9Y7V6 emericella	192	5	10.2	90	9	Q9TLJ5	Q9TLJ5 bacterioph
120	6	12.2	454	2	O53759	O53759 staphylococ	193	5	10.2	90	14	Q9IGQ7	Q9IGQ7 tt virus. o
121	6	12.2	472	2	O53779	Q53779 staphylococ	194	5	10.2	95	5	Q9U712	Q9U712 plasmodium
122	6	12.2	492	2	Q56193	Q56193 staphylococ	195	5	10.2	95	5	Q9U711	Q9U711 plasmodium
123	6	12.2	493	3	Q9UVD1	Q9UVD1 pneumocysti	196	5	10.2	95	5	Q9U710	Q9U710 plasmodium
124	6	12.2	515	5	O76875	O76875 drosophila	197	5	10.2	95	6	Q9U707	Q9U707 monodelphis
125	6	12.2	524	2	O9LCB5	O9LCB5 bacillus su	198	5	10.2	100	5	Q9V6C6	Q9V6C6 drosophila
126	6	12.2	544	1	P95960	P95960 sulfolobus	199	5	10.2	101	2	Q9ZLB3	Q9ZLB3 helicobacte
127	6	12.2	573	2	O56192	Q56192 staphylococ	200	5	10.2	101	2	Q9RQNL	Q9RQNL vibrio chol
128	6	12.2	614	5	O18636	Q18636 caenorhabdi	201	5	10.2	102	8	O35106	Q35106 malaclemys
129	6	12.2	747	2	P94349	P94349 bacillus st	202	5	10.2	102	10	Q9SYR4	Q9SYR4 urtica dioi
130	6	12.2	631	5	Q9W556	Q9W556 drosophila	203	5	10.2	102	10	O9S7L1	O9S7L1 urtica dioi
131	6	12.2	641	2	O9ZJA2	O9ZJA2 helicobacte	204	5	10.2	102	10	O9S7K8	O9S7K8 urtica dioi
132	6	12.2	665	14	O67649	O67649 gibbon ape	205	5	10.2	103	1	Q9YFF7	Q9YFF7 aeropyrum p
133	6	12.2	666	2	O53833	Q53833 staphylococ	206	5	10.2	104	5	O15590	O15590 entamoeba h
134	6	12.2	740	5	Q20760	Q20760 caenorhabdi	207	5	10.2	104	14	O65267	O65267 african swi
135	6	12.2	747	2	O53832	Q53832 staphylococ	208	5	10.2	108	4	O9UDD0	O9UDD0 homo sapien
136	6	12.2	853	5	Q9U019	Q9U019 plasmodium	209	5	10.2	111	8	O9MTN3	O9MTN3 oenothera h
137	6	12.2	1023	3	Q9UOV6	Q9UOV6 yarrowia li	210	5	10.2	116	13	O9YGP3	O9YGP3 ictalurus p
138	6	12.2	1029	10	Q9SUCT9	Q9SUCT9 arabidopsis	211	5	10.2	119	1	Q9UX34	Q9UX34 sulfolobus
139	6	12.2	1199	5	O76570	O76570 caenorhabdi	212	5	10.2	120	2	Q52127	Q52127 lactobacill
140	6	12.2	1232	10	Q9SN91	Q9SN91 arabidopsis	213	5	10.2	120	4	O60519	O60519 homo sapien
141	6	12.2	1249	3	Q00647	Q00647 emericella	214	5	10.2	121	2	O48877	O48877 leptospira
142	6	12.2	1254	14	O41516	O41516 venezuelan	215	5	10.2	121	14	O96671	O96671 chicken ane
143	6	12.2	1254	14	O9YK4	Q9YK4 venezuelan	216	5	10.2	121	14	O39313	O39313 chicken ane
144	6	12.2	1254	14	O9YK8	Q9YK8 venezuelan	217	5	10.2	121	14	O41448	O41448 chicken ane
145	6	12.2	1254	14	Q9YK7	Q9YK7 venezuelan	218	5	10.2	121	14	O9WB33	O9WB33 chicken ane
146	6	12.2	1254	14	Q9WC26	Q9WC26 venezuelan	219	5	10.2	121	14	O9J1K0	O9J1K0 chicken ane
147	6	12.2	1255	14	O66595	O66595 venezuelan	220	5	10.2	121	14	O9IZU6	O9IZU6 chicken ane
148	6	12.2	1255	14	O66593	O66593 venezuelan	221	5	10.2	121	14	O9IEZ4	O9IEZ4 chicken ane
149	6	12.2	1255	14	O90164	O90164 venezuelan	222	5	10.2	122	14	Q9J5E5	Q9J5E5 fowlpox vir
150	6	12.2	1255	14	O91628	O91628 venezuelan	223	5	10.2	123	5	Q27070	Q27070 terebratul
151	6	12.2	1255	14	O36300	O36300 venezuelan	224	5	10.2	123	11	O62379	O62379 mus musculu
152	6	12.2	1255	14	O36288	O36288 venezuelan	225	5	10.2	124	2	O48880	O48880 leptospira
153	6	12.2	1255	14	O98773	O98773 venezuelan	226	5	10.2	124	2	O9RV89	O9RV89 deinococcus
154	6	12.2	1255	14	O98775	O98775 venezuelan	227	5	10.2	124	5	O9W1C9	O9W1C9 drosophila
155	6	12.2	1255	14	Q9WR91	Q9WR91 venezuelan	228	5	10.2	125	3	O9P8P9	O9P8P9 candida alb
156	6	12.2	1255	14	O9WCF8	Q9WCF8 venezuelan	229	5	10.2	125	6	Q9N101	Q9N101 ovis aries
157	6	12.2	1255	14	Q9WCF7	Q9WCF7 venezuelan	230	5	10.2	126	10	Q9XHV7	Q9XHV7 oryza sativ
158	6	12.2	1255	14	Q9WCF6	Q9WCF6 venezuelan	231	5	10.2	127	8	O99275	O99275 centropomus
159	6	12.2	1255	14	O9WCF4	Q9WCF4 venezuelan	232	5	10.2	127	8	O9TG62	O9TG62 centropomus
160	6	12.2	1255	14	O36287	O36287 venezuelan	233	5	10.2	130	8	O9TFP3	O9TFP3 gerris baba
161	6	12.2	1261	2	P73926	P73926 synechocyst	234	5	10.2	130	8	O9TF90	O9TF90 gerris yezo
162	6	12.2	1277	13	O98902	O98902 fugu rubrip	235	5	10.2	130	8	O9TFE9	O9TFE9 gerris yezo
163	6	12.2	1651	5	O45176	O45176 caenorhabdi	236	5	10.2	130	8	O9T9E4	O9T9E4 limnoporus
164	6	12.2	1811	5	Q9XZU8	Q9XZU8 drosophila	237	5	10.2	130	8	O9T9E2	O9T9E2 neogerris p
165	6	12.2	1887	5	Q9VYX6	Q9VYX6 drosophila	238	5	10.2	130	8	O9T9E0	O9T9E0 limnogonus

239	5	10.2	130	8	09T4Q3	09T4Q3	gerria grac	312	5	10.2	175	14	09PZS5	09PZS5	human cytom
240	5	10.2	131	8	09T9F2	09T9F2	gerria nepa	313	5	10.2	175	14	09PZS4	09PZS4	human cytom
241	5	10.2	131	8	09T9F1	09T9F1	gerria nepa	314	5	10.2	175	14	09PZS0	09PZS0	human cytom
242	5	10.2	131	8	09T9E8	09T9E8	aquarius pa	315	5	10.2	175	14	09PZR7	09PZR7	human cytom
243	5	10.2	131	8	09T9E7	09T9E7	aquarius pa	316	5	10.2	175	14	09PZR6	09PZR6	human cytom
244	5	10.2	131	8	09T9E6	09T9E6	aquarius el	317	5	10.2	175	14	09PZR4	09PZR4	human cytom
245	5	10.2	131	8	09T9E5	09T9E5	aquarius el	318	5	10.2	175	14	09PZR3	09PZR3	human cytom
246	5	10.2	131	8	09T9E1	09T9E1	limnogonus	319	5	10.2	175	14	09PZR1	09PZR1	human cytom
247	5	10.2	131	8	09T664	09T664	tenagognus	320	5	10.2	175	14	09PZR0	09PZR0	human cytom
248	5	10.2	131	8	09T434	09T434	gerria lati	321	5	10.2	175	14	09PZQ9	09PZQ9	human cytom
249	5	10.2	131	8	09T320	09T320	gerria insu	322	5	10.2	175	14	09PZQ8	09PZQ8	human cytom
250	5	10.2	132	5	09XWL2	09XWL2	caenorhabdi	323	5	10.2	175	14	09PZQ6	09PZQ6	human cytom
251	5	10.2	133	5	09MGJ7	09MGJ7	microtus lo	324	5	10.2	175	14	09PXA1	09PXA1	human cytom
252	5	10.2	134	5	09YX3	09YX3	hydra magni	325	5	10.2	175	14	09PX94	09PX94	human cytom
253	5	10.2	134	9	09T157	09T157	bacterioph	326	5	10.2	175	14	09PWY0	09PWY0	human cytom
254	5	10.2	136	8	09MGJ9	09MGJ9	microtus lo	327	5	10.2	175	14	09PWX3	09PWX3	human cytom
255	5	10.2	136	8	09MGJ8	09MGJ8	microtus lo	328	5	10.2	176	8	09XLD3	09XLD3	brieniomyr
256	5	10.2	136	8	09MGJ6	09MGJ6	microtus lo	329	5	10.2	177	9	080191	080191	methanobact
257	5	10.2	136	8	09MEZ1	09MEZ1	microtus lo	330	5	10.2	178	2	09Z5J3	09Z5J3	mycobacteri
258	5	10.2	136	8	09MDJ6	09MDJ6	microtus lo	331	5	10.2	178	2	09RN30	09RN30	bacillus an
259	5	10.2	136	14	Q65416	Q65416	beet curly	332	5	10.2	178	2	09JZ22	09JZ22	neisseria m
260	5	10.2	139	4	09NTB6	09NTB6	homo sapien	333	5	10.2	178	10	Q42461	Q42461	canavalia g
261	5	10.2	141	8	09N814	09N814	ixodes hexa	334	5	10.2	178	10	Q42492	Q42492	canavalia g
262	5	10.2	142	2	09S0F8	09S0F8	borrelia bu	335	5	10.2	178	10	Q9SLD4	Q9SLD4	arabidopsis
263	5	10.2	142	2	09R3Z2	09R3Z2	borrelia bu	336	5	10.2	180	8	09XQ15	09XQ15	nuphar adve
264	5	10.2	143	5	09W340	09W340	drosofila	337	5	10.2	181	8	09MIB7	09MIB7	mabuaya affi
265	5	10.2	143	8	09TLV3	09TLV3	cyanidium c	338	5	10.2	181	10	09LYH4	09LYH4	arabidopsis
266	5	10.2	143	10	09SMU5	09SMU5	arabidopsis	339	5	10.2	182	1	Q29054	Q29054	archaeoglob
267	5	10.2	143	10	09MDE2	09MDE2	arabidopsis	340	5	10.2	185	8	09Z2K9	09Z2K9	urosauros m
268	5	10.2	143	14	Q64804	Q64804	autographa	341	5	10.2	185	8	09Z2K8	09Z2K8	petrosaurus
269	5	10.2	144	2	09KJF4	09KJF4	thauera aro	342	5	10.2	185	8	09Z2K7	09Z2K7	uta palmeri
270	5	10.2	146	2	09K7A1	09K7A1	bacillus ha	343	5	10.2	185	8	09Z2K6	09Z2K6	uta stellat
271	5	10.2	154	5	Q15825	Q15825	euplotes oc	344	5	10.2	185	8	09Z2K5	09Z2K5	uta squamat
272	5	10.2	154	5	09VHN3	09VHN3	drosofila	345	5	10.2	185	8	09Z2K4	09Z2K4	uta antiqua
273	5	10.2	155	5	Q61977	Q61977	caenorhabdi	346	5	10.2	185	8	09Z2K3	09Z2K3	uta stansbu
274	5	10.2	157	5	Q9T245	Q9T245	phytothor	347	5	10.2	185	8	09Z2K2	09Z2K2	uta stuejneg
275	5	10.2	158	5	Q23981	Q23981	drosofila	348	5	10.2	185	8	09XQ13	09XQ13	nuphar orbi
276	5	10.2	159	5	Q62289	Q62289	caenorhabdi	349	5	10.2	185	8	09T520	09T520	uta stansbu
277	5	10.2	159	5	Q9U238	Q9U238	caenorhabdi	350	5	10.2	185	8	09T519	09T519	uta stansbu
278	5	10.2	159	6	Q9N1N1	Q9N1N1	papio hamad	351	5	10.2	185	8	09T518	09T518	uta stansbu
279	5	10.2	160	6	Q9N1K0	Q9N1K0	macaca sylv	352	5	10.2	185	8	09T517	09T517	uta stansbu
280	5	10.2	160	14	Q73150	Q73150	human immun	353	5	10.2	185	8	09T516	09T516	uta stansbu
281	5	10.2	162	10	Q42410	Q42410	arabidopsis	354	5	10.2	185	8	09T515	09T515	uta stansbu
282	5	10.2	162	10	Q9LT23	Q9LT23	arabidopsis	355	5	10.2	185	8	09T514	09T514	uta stansbu
283	5	10.2	162	14	Q73147	Q73147	human immun	356	5	10.2	185	8	09T513	09T513	uta stansbu
284	5	10.2	162	14	Q73148	Q73148	human immun	357	5	10.2	185	8	09T512	09T512	uta stansbu
285	5	10.2	164	10	Q9SP66	Q9SP66	arabidopsis	358	5	10.2	185	8	09T511	09T511	uta stansbu
286	5	10.2	166	1	Q59236	Q59236	pyrococcus	359	5	10.2	185	8	09T510	09T510	uta stansbu
287	5	10.2	166	5	Q9VXR8	Q9VXR8	drosofila	360	5	10.2	185	8	09T509	09T509	uta stansbu
288	5	10.2	167	2	Q67858	Q67858	aquifex aeo	361	5	10.2	185	8	09T3A3	09T3A3	uta stansbu
289	5	10.2	167	3	Q9P6L4	Q9P6L4	schizosacch	362	5	10.2	185	8	09T3A2	09T3A2	uta stansbu
290	5	10.2	167	8	Q31757	Q31757	cheloniamy	363	5	10.2	185	8	09MFR7	09MFR7	xenopocellu
291	5	10.2	167	8	Q33371	Q33371	caretta car	364	5	10.2	186	8	09TCB3	09TCB3	nephroselimi
292	5	10.2	167	8	Q33413	Q33413	dermocheley	365	5	10.2	186	9	Q9ZX69	Q9ZX69	mycobacteri
293	5	10.2	167	8	Q33442	Q33442	eretmocheley	366	5	10.2	187	10	Q23132	Q23132	arabidopsis
294	5	10.2	167	8	Q33587	Q33587	lepidocheley	367	5	10.2	188	5	Q9TXQ0	Q9TXQ0	caenorhabdi
295	5	10.2	167	8	Q33588	Q33588	lepidocheley	368	5	10.2	189	8	09MFS8	09MFS8	oryzias cur
296	5	10.2	167	8	Q34068	Q34068	caretta car	369	5	10.2	190	2	09RMV0	09RMV0	bacillus an
297	5	10.2	167	8	Q34158	Q34158	cheloniamy	370	5	10.2	190	2	Q9K284	Q9K284	streptomyce
298	5	10.2	167	8	Q34159	Q34159	cheloniamy	371	5	10.2	191	2	Q9JVL1	Q9JVL1	neisseria m
299	5	10.2	167	8	Q34896	Q34896	lepidocheley	372	5	10.2	191	5	Q9V8X3	Q9V8X3	drosofila
300	5	10.2	167	8	Q36595	Q36595	natafor dep	373	5	10.2	191	8	Q9XL43	Q9XL43	macaca name
301	5	10.2	167	8	Q31754	Q31754	chelydra se	374	5	10.2	191	14	Q98543	Q98543	paramecium
302	5	10.2	169	10	Q9LF91	Q9LF91	arabidopsis	375	5	10.2	194	5	Q62425	Q62425	caenorhabdi
303	5	10.2	171	1	Q9V175	Q9V175	pyrococcus	376	5	10.2	194	8	Q34083	Q34083	coryphaena
304	5	10.2	172	2	Q54789	Q54789	streptococc	377	5	10.2	194	10	Q9MOM9	Q9MOM9	arabidopsis
305	5	10.2	173	11	Q9JKD5	Q9JKD5	rattus norv	378	5	10.2	196	8	Q9XLC2	Q9XLC2	gymnarchus
306	5	10.2	174	10	Q39217	Q39217	arabidopsis	379	5	10.2	196	8	Q9XLB2	Q9XLB2	marcusenius
307	5	10.2	175	4	Q9N285	Q9N285	homo sapien	380	5	10.2	196	8	Q9XLB1	Q9XLB1	pollimyrus
308	5	10.2	175	14	Q9WPM2	Q9WPM2	human cytom	381	5	10.2	196	8	Q9XLA6	Q9XLA6	ivindomyrus
309	5	10.2	175	14	Q9PZS8	Q9PZS8	human cytom	382	5	10.2	196	8	Q9XLA5	Q9XLA5	boulengerom
310	5	10.2	175	14	Q9PZS7	Q9PZS7	human cytom	383	5	10.2	198	2	Q9RCR0	Q9RCR0	streptococc
311	5	10.2	175	14	Q9PZS6	Q9PZS6	human cytom	384	5	10.2	198	2	Q9RCQ5	Q9RCQ5	streptococc

385	5	10.2	198	2	Q9RCQ2	Q9rcq2 streptococc	458	5	10.2	216	8	Q9TAG4	Q9tag4 uma exsul.
386	5	10.2	198	2	Q9RCP8	Q9rcp8 streptococc	459	5	10.2	216	8	Q9TAG3	Q9tag3 uma paraphy
387	5	10.2	198	2	Q9RCM1	Q9rcm1 streptococc	460	5	10.2	217	8	Q9XMK7	Q9xm7 ochotona pr
388	5	10.2	199	10	Q9LWB5	Q9lwb5 spinacia ol	461	5	10.2	217	8	Q9TH74	Q9th74 acomys mino
389	5	10.2	199	5	Q91464	P91464 caenorhabdi	462	5	10.2	217	8	Q9TAH4	Q9tah4 uta stansbu
390	5	10.2	199	8	Q35995	Q35995 tetraapturus	463	5	10.2	217	8	Q9TAH3	Q9tah3 urosaurus o
391	5	10.2	200	2	Q9RG41	Q9rg41 streptococc	464	5	10.2	217	8	Q9TAH2	Q9tah2 urosaurus o
392	5	10.2	201	2	Q9WYN5	Q9wyn5 thermotoga	465	5	10.2	217	8	Q9TAH1	Q9tah1 phrynosoma
393	5	10.2	201	6	Q9TTZ1	Q9ttz1 bos taurus	466	5	10.2	217	8	Q9TAH0	Q9tah0 sceloporus
394	5	10.2	201	10	Q9MLA0	Q9mla0 arabidopsis	467	5	10.2	217	8	Q9TAG9	Q9tag9 sceloporus
395	5	10.2	202	5	Q20534	Q20534 caenorhabdi	468	5	10.2	217	8	Q9TAG8	Q9tag8 callisaurus
396	5	10.2	202	8	Q9MFT0	Q9mft0 oryzias car	469	5	10.2	217	8	Q9TAG7	Q9tag7 callisaurus
397	5	10.2	202	8	Q9MFS1	Q9mfs1 oryzias mek	470	5	10.2	217	8	Q9TAG6	Q9tag6 coposaurus
398	5	10.2	202	10	Q9LW58	Q9lw58 arabidopsis	471	5	10.2	217	8	Q9TAG5	Q9tag5 coposaurus
399	5	10.2	203	2	Q9XBL4	Q9xbl4 bacillus ce	472	5	10.2	217	8	Q9TAG2	Q9tag2 holbrookia
400	5	10.2	203	2	Q9L305	Q9l305 eubacterium	473	5	10.2	217	8	Q9TAG1	Q9tag1 holbrookia
401	5	10.2	203	8	Q36241	Q36241 xiphias gla	474	5	10.2	217	8	Q9TAG0	Q9tag0 holbrookia
402	5	10.2	203	8	Q35978	Q35978 tetraapturus	475	5	10.2	217	8	Q9TAF9	Q9taf9 holbrookia
403	5	10.2	203	8	Q35979	Q35979 tetraapturus	476	5	10.2	217	8	Q9TAF8	Q9taf8 holbrookia
404	5	10.2	203	8	Q35979	Q35979 tetraapturus	477	5	10.2	217	8	Q9TAF7	Q9taf7 holbrookia
405	5	10.2	203	8	Q35008	Q35008 makaira ind	478	5	10.2	217	8	Q9TAF6	Q9taf6 holbrookia
406	5	10.2	203	8	Q35049	Q35049 makaira nig	479	5	10.2	217	8	Q9TAF5	Q9taf5 holbrookia
407	5	10.2	203	8	Q35049	Q35049 makaira nig	480	5	10.2	217	8	Q9TAF4	Q9taf4 holbrookia
408	5	10.2	203	8	Q9MLU9	Q9mlu9 bolitogloss	481	5	10.2	217	8	Q9TAF3	Q9taf3 holbrookia
409	5	10.2	203	8	Q9MLU6	Q9mlu6 bolitogloss	482	5	10.2	217	8	Q9TAF0	Q9taf0 holbrookia
410	5	10.2	203	8	Q9MLB5	Q9mlb5 mabuya eleg	483	5	10.2	217	8	Q9T454	Q9t454 uma scopari
411	5	10.2	203	10	Q9STJ2	Q9stj2 arabidopsis	484	5	10.2	217	8	Q9T3Y7	Q9t3y7 uma notata.
412	5	10.2	204	8	Q36105	Q36105 tetraapturus	485	5	10.2	218	2	Q9KKC0	Q9kkc0 borrelia he
413	5	10.2	204	8	Q9MLU1	Q9mlu1 bolitogloss	486	5	10.2	219	8	Q9XLM9	Q9xlm9 chaicporus
414	5	10.2	204	8	Q9MFS6	Q9mfs6 oryzias jav	487	5	10.2	219	8	Q9TAU5	Q9tau5 strongylura
415	5	10.2	206	8	Q9MLT9	Q9mlt9 bolitogloss	488	5	10.2	219	8	Q9MM62	Q9mm62 adolfus vau
416	5	10.2	206	10	Q9K0W0	Q9m0w0 arabidopsis	489	5	10.2	219	8	Q9MM61	Q9mm61 eremias vel
417	5	10.2	207	8	Q9MLB8	Q9mlb8 bolitogloss	490	5	10.2	219	8	Q9MM60	Q9mm60 nucas tess
418	5	10.2	207	8	Q9MLB4	Q9mlb4 mabuya macu	491	5	10.2	220	2	Q9ZKA5	Q9zka5 helicobacte
419	5	10.2	207	8	Q9MDY2	Q9mdy2 bolitogloss	492	5	10.2	220	2	Q9TAU4	Q9tau4 strongylura
420	5	10.2	208	5	Q9W951	Q9w951 drosophila	493	5	10.2	220	8	Q9T2Y6	Q9t2y6 strongylura
421	5	10.2	210	8	Q9XIV1	Q9xlv1 bolitogloss	494	5	10.2	220	8	Q9MIB1	Q9mib1 mabuya quin
422	5	10.2	210	8	Q99906	Q99906 potamotrygo	495	5	10.2	222	8	Q34402	Q34402 euproctus a
423	5	10.2	210	8	Q9T553	Q9t553 carduelis c	496	5	10.2	222	8	Q34486	Q34486 euproctus m
424	5	10.2	210	8	Q9MFS9	Q9mfs9 oryzias cel	497	5	10.2	222	8	Q34492	Q34492 euproctus p
425	5	10.2	210	8	Q9MFS3	Q9mfs3 oryzias lat	498	5	10.2	222	8	Q35696	Q35696 pleurodeles
426	5	10.2	210	8	Q9MFS3	Q9mfs3 oryzias luz	499	5	10.2	223	1	Q9T578	Q9t578 triturus vu
427	5	10.2	210	8	Q9MFS3	Q9mfs3 oryzias mar	500	5	10.2	223	2	Q9RME7	Q9rme7 zymomonas m
428	5	10.2	210	8	Q9MFS0	Q9mfs0 oryzias nig	501	5	10.2	224	8	Q9XMK6	Q9xm6 zymomonas m
429	5	10.2	210	8	Q9MFS0	Q9mfs0 oryzias nig	502	5	10.2	224	8	Q9TAU3	Q9tau3 pseudotylus
430	5	10.2	210	8	Q9MFR8	Q9mfr8 xenopoeicili	503	5	10.2	224	8	Q9TAU2	Q9tau2 pseudotylus
431	5	10.2	211	8	Q9MFS5	Q9mfs5 oryzias jav	504	5	10.2	224	8	Q9TAU1	Q9tau1 pseudotylus
432	5	10.2	212	10	Q9LWF7	Q9lwf7 oryza sativ	505	5	10.2	224	8	Q9T346	Q9t346 pseudotylus
433	5	10.2	214	2	Q67790	Q67790 aquifex aeo	506	5	10.2	224	8	Q9TAU1	Q9tau1 pseudotylus
434	5	10.2	214	2	P73763	P73763 synechocyst	507	5	10.2	225	8	Q9TAU6	Q9tau6 belonion ap
435	5	10.2	214	8	Q9T554	Q9t554 carduelis c	508	5	10.2	225	8	Q9MIB6	Q9mib6 mabuya cf.
436	5	10.2	214	8	Q9MLU5	Q9mlu5 bolitogloss	509	5	10.2	226	4	Q9KNV6	Q9knv6 vibrio chol
437	5	10.2	214	8	Q9MLU2	Q9mlu2 bolitogloss	510	5	10.2	226	4	Q16018	Q16018 homo sapien
438	5	10.2	215	5	Q20614	Q20614 caenorhabdi	511	5	10.2	226	8	Q9TAV1	Q9tav1 caenorhabdi
439	5	10.2	215	8	Q34237	Q34237 capricornis	512	5	10.2	226	8	Q9TAV1	Q9tav1 potamorrhap
440	5	10.2	215	8	Q34238	Q34238 capricornis	513	5	10.2	226	14	Q9R686	Q9r686 simian cyto
441	5	10.2	215	8	Q35152	Q35152 nemorhaedus	514	5	10.2	227	5	Q69148	Q69148 lactococcus
442	5	10.2	215	8	Q35206	Q35206 oreomys am	515	5	10.2	227	5	Q00924	Q00924 plasmodium
443	5	10.2	215	8	Q35744	Q35744 rupicapra r	516	5	10.2	227	8	Q34432	Q34432 ensatina es
444	5	10.2	215	8	Q34872	Q34872 oryctolagus	517	5	10.2	227	8	Q34433	Q34433 ensatina es
445	5	10.2	215	8	Q9MLV2	Q9mlv2 bolitogloss	518	5	10.2	227	8	Q34434	Q34434 ensatina es
446	5	10.2	215	8	Q9MLV1	Q9mlv1 bolitogloss	519	5	10.2	227	8	Q34435	Q34435 ensatina es
447	5	10.2	215	8	Q9MLV0	Q9mlv0 bolitogloss	520	5	10.2	227	8	Q34437	Q34437 ensatina es
448	5	10.2	215	8	Q9MLU4	Q9mlu4 bolitogloss	521	5	10.2	227	8	Q34438	Q34438 ensatina es
449	5	10.2	215	8	Q9MLU3	Q9mlu3 bolitogloss	522	5	10.2	227	8	Q34439	Q34439 ensatina es
450	5	10.2	215	8	Q9MLU0	Q9mlu0 bolitogloss	523	5	10.2	227	8	Q34440	Q34440 ensatina es
451	5	10.2	215	8	Q9MLT8	Q9mlt8 bolitogloss	524	5	10.2	227	8	Q34441	Q34441 ensatina es
452	5	10.2	215	8	Q9MLT5	Q9mlt5 bolitogloss	525	5	10.2	227	8	Q34442	Q34442 ensatina es
453	5	10.2	215	8	Q9MBC5	Q9mbc5 bolitogloss	526	5	10.2	227	8	Q34443	Q34443 ensatina es
454	5	10.2	215	8	Q9MD02	Q9md02 bolitogloss	527	5	10.2	227	8	Q34444	Q34444 ensatina es
455	5	10.2	216	2	Q9PBU7	Q9pbu7 bolitogloss	528	5	10.2	227	8	Q34445	Q34445 ensatina es
456	5	10.2	216	2	Q9PBU7	Q9pbu7 xyiella fas	529	5	10.2	227	8	Q34446	Q34446 ensatina es
457	5	10.2	216	8	Q36007	Q36007 triturus ca	530	5	10.2	227	8	Q34448	Q34448 ensatina es

531	5	10.2	227	8	Q34449	Q34449 ensatina es	604	5	10.2	238	2	P72818	P72818 synechocyst
532	5	10.2	227	8	Q34450	Q34450 ensatina es	605	5	10.2	238	8	Q03377	Q03377 thryonomys
533	5	10.2	227	8	Q34451	Q34451 ensatina es	606	5	10.2	238	10	Q02901	Q02901 arabidopsis
534	5	10.2	227	8	Q34452	Q34452 ensatina es	607	5	10.2	239	5	Q17769	Q17769 caenorhabdi
535	5	10.2	227	8	Q34453	Q34453 ensatina es	608	5	10.2	239	10	Q98IH3	Q98IH3 arabidopsis
536	5	10.2	227	8	Q35427	Q35427 plethodon e	609	5	10.2	240	2	Q49014	Q49014 mycoplasma
537	5	10.2	228	1	Q9UXX2	Q9UXX2 pyrococcus	610	5	10.2	242	2	Q25560	Q25560 helicobacte
538	5	10.2	228	8	Q9XLV7	Q9XLV7 dascyllus r	611	5	10.2	242	2	Q92KU8	Q92KU8 helicobacte
539	5	10.2	228	8	Q9XLV6	Q9XLV6 dascyllus a	612	5	10.2	243	2	Q69830	Q69830 streptomyce
540	5	10.2	228	8	Q9XLV5	Q9XLV5 dascyllus m	613	5	10.2	243	14	Q09502	Q09502 garlic viru
541	5	10.2	228	8	Q9XLV4	Q9XLV4 dascyllus c	614	5	10.2	244	8	Q34293	Q34293 dasyatis ak
542	5	10.2	228	8	Q9XLV2	Q9XLV2 dascyllus m	615	5	10.2	244	8	Q35520	Q35520 pristic per
543	5	10.2	228	8	Q9XLV0	Q9XLV0 dascyllus t	616	5	10.2	244	8	Q35720	Q35720 rhinobatos
544	5	10.2	228	8	Q9XLU9	Q9XLU9 chromis chr	617	5	10.2	244	8	Q35892	Q35892 squatina ne
545	5	10.2	228	8	Q9TAU7	Q9TAU7 belonion di	618	5	10.2	244	10	Q9LV08	Q9LV08 arabidopsis
546	5	10.2	228	8	Q9MHR8	Q9MHR8 hemidactylu	619	5	10.2	245	8	Q63703	Q63703 batrachosep
547	5	10.2	228	8	Q9MHR7	Q9MHR7 pachydactyl	620	5	10.2	245	5	Q01646	Q01646 drosophila
548	5	10.2	228	8	Q9MHR6	Q9MHR6 tarentola a	621	5	10.2	247	13	Q9RH93	Q9RH93 brachydanio
549	5	10.2	228	8	Q9MHR5	Q9MHR5 tarentola b	622	5	10.2	247	14	P87516	P87516 bovine rota
550	5	10.2	228	8	Q9MHR4	Q9MHR4 tarentola b	623	5	10.2	247	14	P87517	P87517 bovine rota
551	5	10.2	228	8	Q9MHR3	Q9MHR3 tarentola b	624	5	10.2	247	14	P87518	P87518 bovine rota
552	5	10.2	228	8	Q9MHR2	Q9MHR2 tarentola b	625	5	10.2	247	14	Q9WAT1	Q9WAT1 bovine grou
553	5	10.2	228	8	Q9MHR1	Q9MHR1 tarentola d	626	5	10.2	248	3	Q74926	Q74926 schizosacch
554	5	10.2	228	8	Q9MHQ5	Q9MHQ5 tarentola g	627	5	10.2	248	5	Q27458	Q27458 botryllus s
555	5	10.2	228	8	Q9MHQ6	Q9MHQ6 tarentola g	628	5	10.2	249	8	Q9TDQ4	Q9TDQ4 muntiacus f
556	5	10.2	228	8	Q9MHQ4	Q9MHQ4 tarentola g	629	5	10.2	249	8	Q9TDQ3	Q9TDQ3 muntiacus c
557	5	10.2	228	8	Q9MHP7	Q9MHP7 tarentola c	630	5	10.2	250	2	P72645	P72645 synechocyst
558	5	10.2	228	8	Q9MHP6	Q9MHP6 tarentola c	631	5	10.2	250	8	Q9TAV6	Q9TAV6 potamorhaph
559	5	10.2	228	8	Q9MHP5	Q9MHP5 tarentola d	632	5	10.2	250	8	Q9TAV5	Q9TAV5 potamorhaph
560	5	10.2	228	8	Q9MHP4	Q9MHP4 tarentola d	633	5	10.2	250	8	Q9TAV4	Q9TAV4 potamorhaph
561	5	10.2	228	8	Q9MHP3	Q9MHP3 tarentola d	634	5	10.2	250	8	Q9TAV3	Q9TAV3 potamorhaph
562	5	10.2	228	8	Q9MHP2	Q9MHP2 tarentola d	635	5	10.2	250	8	Q9TAV2	Q9TAV2 potamorhaph
563	5	10.2	228	8	Q9MHP1	Q9MHP1 tarentola d	636	5	10.2	250	8	Q9TAV0	Q9TAV0 potamorhaph
564	5	10.2	228	8	Q9MHP0	Q9MHP0 tarentola d	637	5	10.2	250	8	Q9TAF3	Q9TAF3 potamorhaph
565	5	10.2	228	8	Q9MHN9	Q9MHN9 tarentola d	638	5	10.2	250	8	Q9T474	Q9T474 potamorhaph
566	5	10.2	228	8	Q9MHN8	Q9MHN8 tarentola d	639	5	10.2	250	8	Q9T3P2	Q9T3P2 potamorhaph
567	5	10.2	228	8	Q9MHN7	Q9MHN7 tarentola d	640	5	10.2	250	8	Q9T3H3	Q9T3H3 potamorhaph
568	5	10.2	228	8	Q9ME85	Q9ME85 tarentola b	641	5	10.2	251	8	Q63704	Q63704 batrachosep
569	5	10.2	228	8	Q9MDR2	Q9MDR2 tarentola d	642	5	10.2	251	8	Q63707	Q63707 batrachosep
570	5	10.2	228	8	Q9MDN3	Q9MDN3 tarentola c	643	5	10.2	251	11	P70331	P70331 mus musculu
571	5	10.2	228	8	Q9MDG4	Q9MDG4 tarentola d	644	5	10.2	251	14	Q67693	Q67693 garlic viru
572	5	10.2	228	8	Q9MDF7	Q9MDF7 tarentola c	645	5	10.2	252	8	Q99908	Q99908 potamotrygo
573	5	10.2	228	8	Q9MDE2	Q9MDE2 tarentola r	646	5	10.2	252	10	Q9SJB2	Q9SJB2 arabidopsis
574	5	10.2	228	10	Q43308	Q43308 arabidopsis	647	5	10.2	252	14	O12299	O12299 garlic mite
575	5	10.2	229	2	O51423	O51423 borrelia bu	648	5	10.2	253	2	Q32833	Q32833 lactobacill
576	5	10.2	229	2	Q32821	Q32821 legionella	649	5	10.2	253	14	O40643	O40643 salmireline
577	5	10.2	229	8	Q9TBQ2	Q9TBQ2 amphistichu	650	5	10.2	254	1	Q58498	Q58498 methanococc
578	5	10.2	229	8	Q9TBQ1	Q9TBQ1 brachyistiu	651	5	10.2	254	5	Q9VYN7	Q9VYN7 drosophila
579	5	10.2	229	8	Q9TBQ0	Q9TBQ0 cymatogaste	652	5	10.2	254	5	Q9V3J2	Q9V3J2 drosophila
580	5	10.2	229	8	Q9TBP9	Q9TBP9 rhacochilus	653	5	10.2	254	8	Q63705	Q63705 batrachosep
581	5	10.2	229	8	Q9TBP8	Q9TBP8 embiotoca j	654	5	10.2	255	8	Q63706	Q63706 batrachosep
582	5	10.2	229	8	Q9TBP7	Q9TBP7 hyperprosop	655	5	10.2	255	8	Q99904	Q99904 dasyatis ha
583	5	10.2	229	8	Q9TBP6	Q9TBP6 hystero carp	656	5	10.2	255	8	Q99905	Q99905 urobatis ha
584	5	10.2	229	8	Q9TBP5	Q9TBP5 rhacochilus	657	5	10.2	255	8	Q99907	Q99907 potamotrygo
585	5	10.2	229	8	Q9TBP4	Q9TBP4 hypsirus ca	658	5	10.2	255	8	Q99909	Q99909 potamotrygo
586	5	10.2	229	8	Q9TBP3	Q9TBP3 micrometrus	659	5	10.2	255	8	Q99911	Q99911 taenlura ly
587	5	10.2	229	8	Q9TBP2	Q9TBP2 phanerodon	660	5	10.2	255	8	Q99912	Q99912 gymmura mac
588	5	10.2	229	8	Q9TBP1	Q9TBP1 zalembius r	661	5	10.2	255	8	Q99913	Q99913 dasyatis lo
589	5	10.2	229	8	Q9TBP0	Q9TBP0 ditrema tem	662	5	10.2	255	8	Q99914	Q99914 myliobatis
590	5	10.2	229	8	Q9TBN9	Q9TBN9 neoditrema	663	5	10.2	255	8	Q99915	Q99915 rhinoptera
591	5	10.2	229	8	Q9TAU8	Q9TAU8 potamorhaph	664	5	10.2	255	8	Q99916	Q99916 mobula thur
592	5	10.2	230	2	Q9R716	Q9R716 agrobacteri	665	5	10.2	255	8	Q99917	Q99917 plesiotrygo
593	5	10.2	230	2	Q9R699	Q9R699 agrobacteri	666	5	10.2	255	8	Q99918	Q99918 himantura g
594	5	10.2	231	2	Q9RWE4	Q9RWE4 agrobacteri	667	5	10.2	255	8	Q99919	Q99919 himantura p
595	5	10.2	232	2	O31050	O31050 streptococc	668	5	10.2	255	8	Q99920	Q99920 himantura s
596	5	10.2	232	10	Q9MOM3	Q9MOM3 arabidopsis	669	5	10.2	256	2	O68612	O68612 synechococ
597	5	10.2	233	2	O56749	O56749 wolinnella s	670	5	10.2	257	5	Q9VH58	Q9VH58 drosophila
598	5	10.2	233	2	Q9KVJ5	Q9KVJ5 vibrio chol	671	5	10.2	257	8	Q9TEU5	Q9TEU5 apalone spi
599	5	10.2	235	8	Q9TAU9	Q9TAU9 potamorhaph	672	5	10.2	257	8	Q9TEU4	Q9TEU4 apalone spi
600	5	10.2	236	6	Q9N703	Q9N703 cercopitheo	673	5	10.2	257	8	Q9TEU3	Q9TEU3 apalone spi
601	5	10.2	236	6	Q9N0J9	Q9N0J9 saquinus oe	674	5	10.2	257	8	Q9TEU2	Q9TEU2 apalone fer
602	5	10.2	236	11	O62745	O62745 rattus norv	675	5	10.2	257	8	Q9TEU1	Q9TEU1 apalone fer
603	5	10.2	237	8	Q9MM63	Q9MM63 lacerta pat	676	5	10.2	257	8	Q9TEU0	Q9TEU0 apalone mut

677	5	10.2	257	8	Q9TEH9	Q9tet9 apalone mut	750	5	10.2	290	8	Q9TEJ1	Q9tej1 eutropius d
678	5	10.2	257	8	Q9TEH8	Q9tet8 apalone mut	751	5	10.2	292	2	Q9RS12	Q9rs12 deinococcus
679	5	10.2	257	8	Q9T4S7	Q9t4s7 apalone mut	752	5	10.2	292	3	Q9P4C1	Q9p4c1 kluyveromyc
680	5	10.2	257	8	Q9T448	Q9t448 apalone spi	753	5	10.2	294	4	Q9NW22	Q9nw22 homo sapien
681	5	10.2	257	8	Q9T3X6	Q9t3x6 apalone spi	754	5	10.2	295	2	Q54097	Q54097 streptomyce
682	5	10.2	257	8	Q9T3V6	Q9t3v6 apalone spi	755	5	10.2	295	8	Q03320	Q03320 elseyia lati
683	5	10.2	257	10	Q9LRL6	Q9lr16 arabidopsis	756	5	10.2	295	8	Q9TEJ5	Q9tej5 eutropius d
684	5	10.2	257	2	Q9KR23	Q9kr23 vibrio chol	757	5	10.2	295	8	Q9TEJ3	Q9tej3 eutropius d
685	5	10.2	259	4	Q9Y5B2	Q9y5b2 homo sapien	758	5	10.2	296	5	Q19528	Q19528 caenorhabdi
686	5	10.2	259	8	Q48113	Q48113 ramphotyphi	759	5	10.2	296	8	Q9TEJ2	Q9tej2 eutropius d
687	5	10.2	259	10	Q9SG13	Q9sg13 arabidopsis	760	5	10.2	297	5	Q17418	Q17418 caenorhabdi
688	5	10.2	259	14	Q98687	Q98687 simian cyto	761	5	10.2	297	5	Q9NFL9	Q9nfl9 globodera p
689	5	10.2	259	14	Q67661	Q67661 garlic mite	762	5	10.2	297	8	Q47824	Q47824 ocadia sine
690	5	10.2	261	8	Q48088	Q48088 hemidactylu	763	5	10.2	297	8	Q47825	Q47825 cuora auroc
691	5	10.2	262	5	Q9XU29	Q9xu29 caenorhabdi	764	5	10.2	297	8	Q03290	Q03290 clemmys mar
692	5	10.2	263	2	Q78174	Q78174 escherichia	765	5	10.2	297	8	Q03291	Q03291 chelonis my
693	5	10.2	263	4	Q9Y3S5	Q9y3s5 homo sapien	766	5	10.2	297	8	Q03292	Q03292 graptemys p
694	5	10.2	263	8	Q02673	Q02673 himatione s	767	5	10.2	297	8	Q03293	Q03293 geocheleone
695	5	10.2	263	8	Q02674	Q02674 hemignathus	768	5	10.2	297	8	Q03294	Q03294 heosemys sp
696	5	10.2	263	8	Q02675	Q02675 vestliaria c	769	5	10.2	297	8	Q03295	Q03295 tracemys s
697	5	10.2	263	8	Q02676	Q02676 loxops coc	770	5	10.2	297	8	Q03296	Q03296 apalone spi
698	5	10.2	263	8	Q02677	Q02677 oreomystis	771	5	10.2	297	8	Q03301	Q03301 cheilus fimb
699	5	10.2	263	8	Q02678	Q02678 paroreomyza	772	5	10.2	297	8	Q03305	Q03305 carettochel
700	5	10.2	263	8	Q02679	Q02679 hemignathus	773	5	10.2	297	8	Q03312	Q03312 chinemys re
701	5	10.2	263	8	Q02680	Q02680 palmeria do	774	5	10.2	297	8	Q03315	Q03315 chelydra se
702	5	10.2	263	8	Q02681	Q02681 pseudonesto	775	5	10.2	297	8	Q03316	Q03316 dermocheleys
703	5	10.2	263	8	Q02682	Q02682 oreomystis	776	5	10.2	297	8	Q03317	Q03317 dermatemys
704	5	10.2	263	8	Q02683	Q02683 loxia curvi	777	5	10.2	297	8	Q03321	Q03321 kinosternon
705	5	10.2	263	8	Q02684	Q02684 carpodacus	778	5	10.2	297	8	Q03327	Q03327 podocnemis
706	5	10.2	264	8	Q9MM17	Q9mm17 stomatorhin	779	5	10.2	297	8	Q03328	Q03328 phrynosps gi
707	5	10.2	265	3	Q78794	Q78794 schizosacch	780	5	10.2	297	8	Q03335	Q03335 pelusios wi
708	5	10.2	265	3	Q74817	Q74817 schizosacch	781	5	10.2	297	8	Q03339	Q03339 staurotypos
709	5	10.2	265	5	Q9NGC5	Q9ngc5 dictyosteli	782	5	10.2	298	5	Q61736	Q61736 caenorhabdi
710	5	10.2	266	14	Q66793	Q66793 ectromelia	783	5	10.2	298	6	Q9XT56	Q9xt56 bos laurus
711	5	10.2	267	2	Q9KX70	Q9kx70 mycoplasma	784	5	10.2	299	2	Q49149	Q49149 methylobact
712	5	10.2	267	8	Q35149	Q35149 notiomys ed	785	5	10.2	299	4	Q9Y624	Q9y624 homo sapien
713	5	10.2	267	8	Q02951	Q02951 damaliscus	786	5	10.2	299	8	Q9THC4	Q9thc4 lemmus sibi
714	5	10.2	267	8	Q02950	Q02950 gazella gra	787	5	10.2	300	1	Q28459	Q28459 archaeoglob
715	5	10.2	267	14	Q87048	Q87048 semliki for	788	5	10.2	300	4	Q00121	Q00121 homo sapien
716	5	10.2	268	4	Q9UJD4	Q9ujd4 homo sapien	789	5	10.2	300	8	Q02828	Q02828 sauromalus
717	5	10.2	268	1	Q9S886	Q9s886 sulfolobus	790	5	10.2	300	8	Q02829	Q02829 sauromalus
718	5	10.2	269	5	Q9VFA5	Q9vfa5 drosophila	791	5	10.2	300	8	Q02830	Q02830 sauromalus
719	5	10.2	269	14	Q41125	Q41125 paramacium	792	5	10.2	300	8	Q02831	Q02831 sauromalus
720	5	10.2	270	5	Q9N364	Q9n364 caenorhabdi	793	5	10.2	300	8	Q02832	Q02832 sauromalus
721	5	10.2	270	10	Q9LT67	Q9lt67 arabidopsis	794	5	10.2	300	8	Q02833	Q02833 sauromalus
722	5	10.2	271	8	Q9T3K5	Q9t3k5 gallotia si	795	5	10.2	300	8	Q02834	Q02834 sauromalus
723	5	10.2	271	8	Q9T3K4	Q9t3k4 gallotia si	796	5	10.2	300	8	Q02835	Q02835 sauromalus
724	5	10.2	272	2	Q45329	Q45329 brucella ov	797	5	10.2	300	8	Q02836	Q02836 sauromalus
725	5	10.2	273	2	Q9ZCC1	Q9zcc1 rickettsia	798	5	10.2	300	8	Q02837	Q02837 sauromalus
726	5	10.2	273	3	Q94670	Q94670 schizosacch	799	5	10.2	300	8	Q02838	Q02838 sauromalus
727	5	10.2	273	5	Q76688	Q76688 caenorhabdi	800	5	10.2	300	8	Q02839	Q02839 sauromalus
728	5	10.2	274	2	Q9PNE8	Q9pne8 campylobact	801	5	10.2	300	8	Q02840	Q02840 sauromalus
729	5	10.2	274	3	Q04396	Q04396 saccharomyc	802	5	10.2	300	8	Q02841	Q02841 sauromalus
730	5	10.2	275	1	Q28963	Q28963 archaeoglob	803	5	10.2	300	8	Q02842	Q02842 sauromalus
731	5	10.2	275	5	Q9VZB9	Q9vzb9 drosophila	804	5	10.2	300	8	Q02843	Q02843 sauromalus
732	5	10.2	275	10	Q9SAJ8	Q9saj8 arabidopsis	805	5	10.2	300	8	Q02844	Q02844 sauromalus
733	5	10.2	276	2	Q9S3R6	Q9s3r6 porphyromon	806	5	10.2	300	8	Q02845	Q02845 sauromalus
734	5	10.2	276	3	Q36033	Q36033 schizosacch	807	5	10.2	300	8	Q02846	Q02846 sauromalus
735	5	10.2	276	5	Q9VFE6	Q9vfe6 drosophila	808	5	10.2	300	8	Q02847	Q02847 ctenosaura
736	5	10.2	276	8	Q9MM44	Q9mm44 brienomyrus	809	5	10.2	300	8	Q02848	Q02848 cyclura nub
737	5	10.2	279	2	Q9X1F1	Q9x1f1 thermotoga	810	5	10.2	300	8	Q02849	Q02849 dipsosaurus
738	5	10.2	282	1	Q21964	Q21964 caenorhabdi	811	5	10.2	300	8	Q02850	Q02850 conolophus
739	5	10.2	282	1	Q58835	Q58835 methanococc	812	5	10.2	300	8	Q21739	Q21739 sauromalus
740	5	10.2	283	10	Q9SJB6	Q9sjb6 arabidopsis	813	5	10.2	300	8	Q21771	Q21771 sauromalus
741	5	10.2	284	5	Q9W3F6	Q9w3f6 drosophila	814	5	10.2	300	8	Q21776	Q21776 sauromalus
742	5	10.2	284	14	Q42087	Q42087 equine herp	815	5	10.2	300	8	Q21779	Q21779 sauromalus
743	5	10.2	285	2	Q9KMC9	Q9kmc9 vibrio chol	816	5	10.2	300	8	Q33966	Q33966 brachylophu
744	5	10.2	285	4	Q43608	Q43608 homo sapien	817	5	10.2	300	8	Q9THC5	Q9thc5 lemmus sibi
745	5	10.2	285	8	P92814	P92814 paralichthy	818	5	10.2	300	11	Q88792	Q88792 mus musculu
746	5	10.2	286	2	Q9R640	Q9r640 mycobacteri	819	5	10.2	300	11	Q9JHY1	Q9jhy1 rattus norv
747	5	10.2	286	5	Q18004	Q18004 caenorhabdi	820	5	10.2	302	2	Q9X9Y3	Q9x9y3 streptomyce
748	5	10.2	286	5	Q9U018	Q9u018 plasmodium d	821	5	10.2	302	3	P87106	P87106 pneumocysti
749	5	10.2	290	8	Q9TEJ4	Q9tej4 eutropius d	822	5	10.2	302	3	Q04110	Q04110 saccharomyc

823	5	10.2	302	5	Q21937	Q21937 caenorhabdi	896	5	10.2	332	2	P71945	P71945 mycobacteri
824	5	10.2	303	8	Q92ZV2	Q92zv2 lenmus trim	897	5	10.2	332	2	Q9JUW5	Q9juw5 neisseria m
825	5	10.2	303	10	Q9XTH1	Q9xth1 arabidopsis	898	5	10.2	332	10	Q9M510	Q9m510 lycopersico
826	5	10.2	304	2	Q9PJ91	Q9pj91 campylobact	899	5	10.2	332	10	Q9LUA2	Q9lua2 arabidopsis
827	5	10.2	304	5	Q21579	Q21579 caenorhabdi	900	5	10.2	332	14	Q9Q8C1	Q9qbc1 yaba monkey
828	5	10.2	304	10	Q22140	Q22140 arabidopsis	901	5	10.2	334	2	Q9PHS9	Q9phs9 campylobact
829	5	10.2	304	10	Q9LPY1	Q9lpy1 arabidopsis	902	5	10.2	335	2	Q9RGU4	Q9rgu4 salmonella
830	5	10.2	305	2	Q9PQ27	Q9pq27 ureaplasma	903	5	10.2	335	4	Q9NZ56	Q9nz56 homo sapien
831	5	10.2	305	8	Q92ZV6	Q92zv6 lenmus sibi	904	5	10.2	335	8	Q03383	Q03383 trichechus
832	5	10.2	305	8	Q92ZV5	Q92zv5 lenmus sibi	905	5	10.2	335	8	Q09233	Q09233 hydrotomali
833	5	10.2	305	8	Q92ZV4	Q92zv4 lenmus sibi	906	5	10.2	335	8	Q92Y31	Q92y31 elephantulu
834	5	10.2	305	8	Q92ZV3	Q92zv3 lenmus trim	907	5	10.2	336	1	Q27597	Q27597 methanobact
835	5	10.2	305	8	Q92ZV1	Q92zv1 lenmus sibi	908	5	10.2	336	2	Q51135	Q51135 borrelia bu
836	5	10.2	306	8	Q34412	Q34412 emoiia caeru	909	5	10.2	336	3	Q94150	Q94150 candida alb
837	5	10.2	307	10	Q80577	Q80577 arabidopsis	910	5	10.2	336	8	Q79424	Q79424 neomys anom
838	5	10.2	308	9	Q38096	Q38096 bacterioph	911	5	10.2	336	8	Q9XMF1	Q9xmf1 acomys sp.
839	5	10.2	309	1	Q58333	Q58333 pyrococcus	912	5	10.2	336	8	Q9TH77	Q9th77 acomys sp.
840	5	10.2	309	2	Q51695	Q51695 borrelia bu	913	5	10.2	337	10	Q9SGD1	Q9sgd1 arabidopsis
841	5	10.2	309	8	Q34413	Q34413 emoiia cyanu	914	5	10.2	337	14	Q55820	Q55820 rio bravo v
842	5	10.2	309	10	Q9SN79	Q9sn79 arabidopsis	915	5	10.2	340	2	Q9RDV6	Q9rdv6 mycoplasma
843	5	10.2	310	1	Q28615	Q28615 archaeoglob	916	5	10.2	340	5	Q23672	Q23672 caenorhabdi
844	5	10.2	310	2	Q45414	Q45414 bacillus sp	917	5	10.2	340	8	Q9TEE3	Q9tee3 schilbe int
845	5	10.2	310	5	Q94389	Q94389 caenorhabdi	918	5	10.2	340	8	Q9SUX8	Q9sux8 arabidopsis
846	5	10.2	311	5	Q9N768	Q9n768 leishmania	919	5	10.2	341	2	P72894	P72894 synechocyst
847	5	10.2	311	8	Q95789	Q95789 emoiia cyanu	920	5	10.2	341	5	Q9VT93	Q9vt93 drosophila
848	5	10.2	311	8	Q95790	Q95790 emoiia cyanu	921	5	10.2	341	5	Q9VR72	Q9vr72 drosophila
849	5	10.2	311	8	Q95791	Q95791 emoiia cyanu	922	5	10.2	342	3	Q9P5N5	Q9p5n5 neurospora
850	5	10.2	311	8	Q95792	Q95792 emoiia cyanu	923	5	10.2	342	8	Q9TEE2	Q9tee2 schilbe int
851	5	10.2	311	8	Q95794	Q95794 emoiia impar	924	5	10.2	343	10	Q9M519	Q9m519 populus alb
852	5	10.2	311	8	Q95795	Q95795 emoiia impar	925	5	10.2	345	8	Q9MJT2	Q9mjt2 emys orbicu
853	5	10.2	311	8	Q95796	Q95796 emoiia isola	926	5	10.2	345	8	Q9MJT1	Q9mjt1 emys orbicu
854	5	10.2	311	8	Q95798	Q95798 emoiia impar	927	5	10.2	345	8	Q9MJT0	Q9mjt0 emys orbicu
855	5	10.2	311	8	Q95799	Q95799 emoiia impar	928	5	10.2	345	8	Q9MJS9	Q9mjs9 emys orbicu
856	5	10.2	311	8	Q95800	Q95800 emoiia impar	929	5	10.2	345	8	Q9MJS8	Q9mjs8 terrapene o
857	5	10.2	311	8	Q95805	Q95805 emoiia pseud	930	5	10.2	345	8	Q9MJS7	Q9mjs7 clemmys ins
858	5	10.2	311	8	Q95806	Q95806 emoiia pseud	931	5	10.2	345	8	Q9MJS6	Q9mjs6 clemmys gut
859	5	10.2	311	8	Q96115	Q96115 emoiia cyanu	932	5	10.2	345	8	Q9MJS5	Q9mjs5 clemmys mar
860	5	10.2	311	8	Q34411	Q34411 emoiia cyanu	933	5	10.2	345	8	Q9MJS4	Q9mjs4 clemmys muh
861	5	10.2	311	8	Q34414	Q34414 emoiia cyanu	934	5	10.2	345	8	Q9MJS3	Q9mjs3 emydolidea b
862	5	10.2	311	8	Q34465	Q34465 emoiia impar	935	5	10.2	345	8	Q9MJS2	Q9mjs2 emys orbicu
863	5	10.2	311	8	Q34466	Q34466 emoiia impar	936	5	10.2	345	8	Q9MDP0	Q9mdp0 emys orbicu
864	5	10.2	312	10	Q9MIF0	Q9mif0 arabidopsis	937	5	10.2	345	8	Q9MDC5	Q9mdc5 emys orbicu
865	5	10.2	314	2	Q9KAC3	Q9kac3 helicobacte	938	5	10.2	345	8	Q9MDA7	Q9mda7 emys orbicu
866	5	10.2	315	2	Q9KAC6	Q9kac6 bacillus ha	939	5	10.2	345	8	Q9MDA6	Q9mda6 emys orbicu
867	5	10.2	318	10	Q23303	Q23303 arabidopsis	940	5	10.2	345	14	Q66098	Q66098 carnation r
868	5	10.2	318	10	Q9LYE2	Q9lye2 arabidopsis	941	5	10.2	346	2	Q48391	Q48391 klebsiella
869	5	10.2	319	5	Q20054	Q20054 caenorhabdi	942	5	10.2	347	8	Q63399	Q63399 chlorochrys
870	5	10.2	319	11	Q9JKA5	Q9jka5 mus musculu	943	5	10.2	347	8	Q63401	Q63401 chlorophoni
871	5	10.2	320	3	Q13842	Q13842 schizosacch	944	5	10.2	347	8	Q63406	Q63406 cissopsis le
872	5	10.2	320	5	Q45814	Q45814 caenorhabdi	945	5	10.2	347	8	Q63409	Q63409 creurgops d
873	5	10.2	321	8	Q99260	Q99260 damaliscus	946	5	10.2	347	8	Q63413	Q63413 delothraupi
874	5	10.2	322	5	Q21471	Q21471 caenorhabdi	947	5	10.2	347	8	Q63417	Q63417 euphonia la
875	5	10.2	323	5	Q9VWH9	Q9vwh9 drosophila	948	5	10.2	347	8	Q63422	Q63422 iridosornis
876	5	10.2	324	2	Q56699	Q56699 vibrio harv	949	5	10.2	347	8	Q63427	Q63427 neothraupis
877	5	10.2	324	8	Q79326	Q79326 capra ibex	950	5	10.2	347	8	Q63431	Q63431 pipraeidea
878	5	10.2	325	5	Q21104	Q21104 caenorhabdi	951	5	10.2	347	8	Q63438	Q63438 tangara gyr
879	5	10.2	325	5	Q23244	Q23244 caenorhabdi	952	5	10.2	347	8	Q63928	Q63928 schistochia
880	5	10.2	326	2	Q45727	Q45727 bacillus th	953	5	10.2	347	8	Q99250	Q99250 piranga rub
881	5	10.2	326	10	Q9M826	Q9m826 arabidopsis	954	5	10.2	347	8	Q21634	Q21634 lacerta med
882	5	10.2	327	10	Q9LVB2	Q9lvb2 arabidopsis	955	5	10.2	347	8	Q9TB31	Q9tb31 okapia john
883	5	10.2	329	8	Q79321	Q79321 capra ibex	956	5	10.2	347	8	Q9MM81	Q9mm81 algyroides
884	5	10.2	329	8	Q79328	Q79328 capra pyren	957	5	10.2	347	8	Q9MM80	Q9mm80 lacerta mon
885	5	10.2	329	8	Q79329	Q79329 capra pyren	958	5	10.2	347	8	Q9MM79	Q9mm79 podarcis si
886	5	10.2	329	8	Q9T583	Q9t583 capra pyren	959	5	10.2	347	8	Q9MM78	Q9mm78 ophisops el
887	5	10.2	329	8	Q9T582	Q9t582 capra pyren	960	5	10.2	347	8	Q9MM77	Q9mm77 takydromus
888	5	10.2	329	8	Q9T4F5	Q9t4f5 capra pyren	961	5	10.2	347	8	Q9MM76	Q9mm76 gallotia ga
889	5	10.2	329	8	Q9T342	Q9t342 capra pyren	962	5	10.2	347	8	Q9MM75	Q9mm75 psammodromu
890	5	10.2	330	2	Q07474	Q07474 staphylococ	963	5	10.2	347	8	Q9MM74	Q9mm74 acanthodact
891	5	10.2	330	2	Q07859	Q07859 staphylococ	964	5	10.2	347	8	Q9MM73	Q9mm73 lacerta and
892	5	10.2	331	2	Q9PMD1	Q9pmd1 campylobact	965	5	10.2	347	8	Q9MM71	Q9mm71 adolfus jac
893	5	10.2	331	5	Q97262	Q97262 plasmodium	966	5	10.2	347	8	Q9MM70	Q9mm70 meroles sub
894	5	10.2	331	10	Q39954	Q39954 hellanthus	967	5	10.2	347	8	Q9MM69	Q9mm69 tropidosaur
895	5	10.2	332	1	Q27009	Q27009 methanobact	968	5	10.2	347	8	Q9MM66	Q9mm66 hellibolus

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969 5 10.2 347 8 Q9MM65 Q9mm65 latastia lo
970 5 10.2 347 8 Q9MM64 Q9mm64 pedicoplanis
971 5 10.2 347 10 Q82063 Q82063 solanum tub
972 5 10.2 348 8 Q95777 Q95777 catagonus w
973 5 10.2 348 8 Q95935 Q95935 tayassu taj
974 5 10.2 348 8 Q95962 Q95962 tayassu pec
975 5 10.2 349 1 Q74028 Q74028 methanobact
976 5 10.2 349 2 Q71492 Q71492 mycoplasma
977 5 10.2 349 2 Q9PCN2 Q9pcn2 xylella fas
978 5 10.2 350 5 Q20618 Q20618 caenorhabdi
979 5 10.2 350 10 Q82279 Q82279 arabidopsis
980 5 10.2 351 10 Q9SXX6 Q9sxx6 nicotiana t
981 5 10.2 352 2 Q9KXZ1 Q9kxz1 arabidopsis
982 5 10.2 352 8 Q9TF44 Q9tf44 vibrio chol
983 5 10.2 352 13 Q9PSU8 Q9psu8 oryctolagus
984 5 10.2 353 5 Q21051 Q21051 oryctolagus lat
985 5 10.2 353 8 Q9TE69 Q9te69 caenorhabdi
986 5 10.2 353 8 Q9TE65 Q9te65 fragilaria
987 5 10.2 354 10 Q04440 Q04440 thalassione
988 5 10.2 355 8 Q9W009 Q9w009 streptomyce
989 5 10.2 355 8 Q9TEF8 Q9tef8 oryctolagus
990 5 10.2 357 4 Q9NWS6 Q9nws6 homo sapien
991 5 10.2 358 2 Q9PHI3 Q9phi3 campylobact
992 5 10.2 358 4 Q75769 Q75769 homo sapien
993 5 10.2 359 2 Q9KHV8 Q9khv8 rhizobium m
994 5 10.2 359 4 Q13394 Q13394 homo sapien
995 5 10.2 359 5 Q9Y586 Q9y586 homo sapien
996 5 10.2 359 5 Q62031 Q62031 caenorhabdi
997 5 10.2 359 5 Q20880 Q20880 caenorhabdi

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ALIGNMENTS

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RESULT 1
Q9YVB3 ID Q9YVB3 PRELIMINARY; PRT; 293 AA.
AC Q9YVB3;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE ATTACHMENT GLYCOPROTEIN G (FRAGMENT)
OS Human respiratory syncytial virus
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=VV6973;
RX MEDLINE=99022964; PubMed=9806017;
RA Sullender W.M., Mufson M.A., Prince G., Anderson L.J., Wertz G.W.;
RT "Antigenic and genetic diversity among the attachment proteins of
RT group A respiratory syncytial viruses that have caused repeat
RT infections in children."
RL J. Infect. Dis. 178:925-932(1998).
DR EMBL; AF065407; AAD02943.1; -.
DR INTERPRO; IPR000255; -.
DR INTERPRO; IPR000925; -.
DR INTERPRO; IPR002965; -.
DR PFAM; PF00802; Glycoprotein G; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR PROSITE; PS00012; PHOSPHOPANTHEINE; UNKNOWN_1.
FT NON_TER
SQ SEQUENCE 293 AA; 32125 MW; 17B5B43396A63CCF CRC64;

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Query Match 100.0%; Score 49; DB 14; Length 293;
Best Local Similarity 100.0%; Pred. No. 3.le-46;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 KQONKPPSKPNDFHFVFNFPVPCISCSNNPTCWAICKRIPNKKPGK 49
Db 144 KQONKPPSKPNDFHFVFNFPVPCISCSNNPTCWAICKRIPNKKPGK 192

RESULT 2
Q9YVB2 ID Q9YVB2 PRELIMINARY; PRT; 292 AA.
AC Q9YVB2;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE ATTACHMENT GLYCOPROTEIN G (FRAGMENT)
OS Human respiratory syncytial virus
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=VV19983;
RX MEDLINE=99022964; PubMed=9806017;
RA Sullender W.M., Mufson M.A., Prince G., Anderson L.J., Wertz G.W.;
RT "Antigenic and genetic diversity among the attachment proteins of
RT group A respiratory syncytial viruses that have caused repeat
RT infections in children."
RL J. Infect. Dis. 178:925-932(1998).
DR EMBL; AF065408; AAD02944.1; -.
DR INTERPRO; IPR000255; -.
DR INTERPRO; IPR000925; -.
DR INTERPRO; IPR002965; -.
DR PFAM; PF00802; Glycoprotein G; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR PROSITE; PS00012; PHOSPHOPANTHEINE; UNKNOWN_1.
FT NON_TER
SQ SEQUENCE 292 AA; 31964 MW; 8942A8DD0A402A4B CRC64;

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Query Match 98.0%; Score 48; DB 14; Length 292;
Best Local Similarity 100.0%; Pred. No. 3.9e-45;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 KQONKPPSKPNDFHFVFNFPVPCISCSNNPTCWAICKRIPNKKPGK 48
Db 144 KQONKPPSKPNDFHFVFNFPVPCISCSNNPTCWAICKRIPNKKPGK 191

RESULT 3
Q86356 ID Q86356 PRELIMINARY; PRT; 295 AA.
AC Q86356;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE G PROTEIN (FRAGMENT)
OS respiratory syncytial virus
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=12814;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=RSB89-1734;
RX MEDLINE=91374005; PubMed=1895054;
RA Cane P.A., Matthews D.A., Pringle C.R.;
RT "Identification of variable domains of the attachment (G) protein of
RT subgroup A respiratory syncytial viruses."
RL J. Gen. Virol. 72:2091-2096(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=RSB89-1734;
RX Cane P.A.;
RL Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; X73350; CAA51761.1; -.
DR INTERPRO; IPR000255; -.

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DR INTERPRO: IPR000925; -.
DR PFAM: PF00802; Glycoprotein_G; 1.
DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 295 AA; 32527 MW; D32BE769E0A23CEFA CRC64;

Query Match 98.0%; Score 48; DB 14; Length 295;
Best Local Similarity 100.0%; Pred. No. 4e-45;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQKQKPPSKPNDFHFEVFNFPVCSICSNNTPTCWAICKRIPNKKPGK 48
Db 147 KQKQKPPSKPNDFHFEVFNFPVCSICSNNTPTCWAICKRIPNKKPGK 194

RESULT 4
Q86360
ID Q86360 PRELIMINARY; PRT; 295 AA.
AC Q86360;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE G PROTEIN (FRAGMENT);
OS Respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=12814;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RSB89-642;
RX MEDLINE=91374095; PubMed=1895054;
RA Cane P.A., Matthews D.A., Pringle C.R.;
RT "Identification of variable domains of the attachment (G) protein of
RT subgroup A respiratory syncytial viruses.";
RL J. Gen. Virol. 72:2091-2096(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=RSB89-642;
RA Cane P.A.;
RL Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL: X73354; CAA51765.1; -.
DR INTERPRO: IPR000255; -.
DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 295 AA; 32306 MW; 671DCF044157D284 CRC64;

Query Match 98.0%; Score 48; DB 14; Length 295;
Best Local Similarity 100.0%; Pred. No. 4e-45;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQKQKPPSKPNDFHFEVFNFPVCSICSNNTPTCWAICKRIPNKKPGK 48
Db 147 KQKQKPPSKPNDFHFEVFNFPVCSICSNNTPTCWAICKRIPNKKPGK 194

RESULT 5
Q82066
ID Q82066 PRELIMINARY; PRT; 297 AA.
AC Q82066;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE GLYCOPROTEIN.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
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RP SEQUENCE FROM N.A.
RC STRAIN=SUBGROUP A;
RX MEDLINE=94335057; PubMed=8057427;
RA Garcia O., Martin M., Dopazo J., Arbiza J., Fabrasile S., Russi J.,
RA Hortal M., Perez-Brena P., Martinez I., Garcia-Barreno B.,
RA Melero J.A.;
RT "Evolutionary pattern of human respiratory syncytial virus (subgroup
RT A): cocirculating lineages and correlation of genetic and antigenic
RL J. Virol. 68:5448-5459(1994).
DR EMBL: Z33427; CAA83870.1; -.
DR INTERPRO: IPR000255; -.
DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
SQ SEQUENCE 297 AA; 32589 MW; F210F8C68193F5DD CRC64;

Query Match 98.0%; Score 48; DB 14; Length 297;
Best Local Similarity 100.0%; Pred. No. 4e-45;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQKQKPPSKPNDFHFEVFNFPVCSICSNNTPTCWAICKRIPNKKPGK 48
Db 149 KQKQKPPSKPNDFHFEVFNFPVCSICSNNTPTCWAICKRIPNKKPGK 196

RESULT 6
Q82067
ID Q82067 PRELIMINARY; PRT; 297 AA.
AC Q82067;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE GLYCOPROTEIN.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SUBGROUP A;
RX MEDLINE=94335057; PubMed=8057427;
RA Garcia O., Martin M., Dopazo J., Arbiza J., Fabrasile S., Russi J.,
RA Hortal M., Perez-Brena P., Martinez I., Garcia-Barreno B.,
RA Melero J.A.;
RT "Evolutionary pattern of human respiratory syncytial virus (subgroup
RT A): cocirculating lineages and correlation of genetic and antigenic
RL J. Virol. 68:5448-5459(1994).
DR EMBL: Z33428; CAA83871.1; -.
DR INTERPRO: IPR000255; -.
DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
SQ SEQUENCE 297 AA; 32555 MW; 9D0A69BECAB8B6C8 CRC64;

Query Match 98.0%; Score 48; DB 14; Length 297;
Best Local Similarity 100.0%; Pred. No. 4e-45;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQKQKPPSKPNDFHFEVFNFPVCSICSNNTPTCWAICKRIPNKKPGK 48
Db 149 KQKQKPPSKPNDFHFEVFNFPVCSICSNNTPTCWAICKRIPNKKPGK 196

RESULT 7
Q82071
ID Q82071 PRELIMINARY; PRT; 297 AA.
AC Q82071;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
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DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE GLYCOPROTEIN.
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SUBGROUP A;
RX MEDLINE=94335057; PubMed=8057427;
RA Garcia O., Martin M., Dopazo J., Arbiza J., Fabrasile S., Russi J.,
RA Hortal M., Perez-Brena P., Martinez I., Garcia-Barreno B.,
RA Melero J.A.;
RT "Evolutionary pattern of human respiratory syncytial virus (subgroup
A): cocirculating lineages and correlation of genetic and antigenic
changes in the G glycoprotein.";
RL J. Virol. 68:5448-5459(1994).
DR EMBL; Z33432; CAA83875.1; -;
DR INTERPRO; IPR000255; -;
DR INTERPRO; IPR000925; -;
DR PFAM; PF00802; Glycoprotein_G; 1.
DR PROSITE; PS00012; PHOSPHOPANTHEINE; UNKNOWN_1.
SQ SEQUENCE 297 AA; 32581 MW; AD947B2318193306 CRC64;

Query Match 98.08; Score 48; DB 14; Length 297;
Best Local Similarity 100.0%; Pred. No. 4e-45; Indels 0; Gaps 0;
Matches 48; Conservative 0; Mismatches 0;

QY 1 KORONKPPSPNDFHEVFVPCSCSNNPTCWAICKRIPNKKPGK 48
|||||
DB 149 KORONKPPSPNDFHEVFVPCSCSNNPTCWAICKRIPNKKPGK 196

RESULT 8
ID Q9YVB5 PRELIMINARY; PRT; 297 AA.
AC Q9YVB5;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE ATTACHMENT GLYCOPROTEIN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WV2780;
RX MEDLINE=99022964; PubMed=9806017;
RA Sullender W.M., Mufson M.A., Prince G., Anderson L.J., Wertz G.W.;
RT "Antigenic and genetic diversity among the attachment proteins of
group A respiratory syncytial viruses that have caused repeat
infections in children.";
RL J. Infect. Dis. 178:925-932(1998).
DR EMBL; AF065405; AAD02941.1; -;
DR INTERPRO; IPR000255; -;
DR INTERPRO; IPR000925; -;
DR INTERPRO; IPR002965; -;
DR PFAM; PF00802; Glycoprotein_G; 1.
DR PRINTS; PR01217; PRICEXTENS.
DR PROSITE; PS00012; PHOSPHOPANTHEINE; UNKNOWN_1.
SQ SEQUENCE 297 AA; 32572 MW; 5C10E719A05EF5C1 CRC64;

Query Match 98.08; Score 48; DB 14; Length 297;
Best Local Similarity 100.0%; Pred. No. 4e-45; Indels 0; Gaps 0;
Matches 48; Conservative 0; Mismatches 0;

QY 1 KORONKPPSPNDFHEVFVPCSCSNNPTCWAICKRIPNKKPGK 48
|||||

DB 149 KORONKPPSPNDFHEVFVPCSCSNNPTCWAICKRIPNKKPGK 196
RESULT 9
ID Q91947 PRELIMINARY; PRT; 297 AA.
AC Q91947;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE ATTACHMENT PROTEIN.
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CH34;
RX MEDLINE=98418504; PubMed=9747732;
RA Peret T.C.F., Hall C.B., Schnabel K.C., Golub J.A., Anderson L.J.;
RT "Circulation patterns of genetically distinct group A and B strains of
human respiratory syncytial virus in a community.";
RL J. Gen. Virol. 79:2221-2229(1998).
DR EMBL; AF065257; AAC36327.1; -;
DR INTERPRO; IPR000255; -;
DR INTERPRO; IPR000925; -;
DR PFAM; PF00802; Glycoprotein_G; 1.
DR PROSITE; PS00012; PHOSPHOPANTHEINE; UNKNOWN_1.
SQ SEQUENCE 297 AA; 32564 MW; 377C7CBC0D0A3645 CRC64;

Query Match 85.78; Score 42; DB 14; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.6e-38; Indels 0; Gaps 0;
Matches 42; Conservative 0; Mismatches 0;

QY 7 PPSKPNDHFHEVFVPCSCSNNPTCWAICKRIPNKKPGK 48
|||||
DB 155 PPSKPNDHFHEVFVPCSCSNNPTCWAICKRIPNKKPGK 196

RESULT 10
ID Q82070 PRELIMINARY; PRT; 297 AA.
AC Q82070;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE ATTACHMENT GLYCOPROTEIN.
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SUBGROUP A;
RX MEDLINE=94335057; PubMed=8057427;
RA Garcia O., Martin M., Dopazo J., Arbiza J., Fabrasile S., Russi J.,
RA Hortal M., Perez-Brena P., Martinez I., Garcia-Barreno B.,
RA Melero J.A.;
RT "Evolutionary pattern of human respiratory syncytial virus (subgroup
A): cocirculating lineages and correlation of genetic and antigenic
changes in the G glycoprotein.";
RL J. Virol. 68:5448-5459(1994).
DR EMBL; Z33431; CAA83874.1; -;
DR INTERPRO; IPR000255; -;
DR INTERPRO; IPR000925; -;
DR PFAM; PF00802; Glycoprotein_G; 1.
DR PROSITE; PS00012; PHOSPHOPANTHEINE; UNKNOWN_1.
SQ SEQUENCE 297 AA; 32518 MW; EE913CBF1259BB8 CRC64;

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Query Match      83.7%; Score 41; DB 14; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.9e-37;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PSKNNDFHFEVFNPCSCSNNPTCWAICKRIPNKKPGK 48
    |||||
Db 156 PSKNNDFHFEVFNPCSCSNNPTCWAICKRIPNKKPGK 196

RESULT 11
Q906U1 ID Q906U1 PRELIMINARY; PRT; 278 AA.
AC Q906U1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE GLYCOPROTEIN (FRAGMENT).
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=91142;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroup A and B respiratory syncytial viruses isolated over nine
RT consecutive epidemics.";
RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF193305; AAF23728.1;
DR INTERPRO; IPR000255;
DR INTERPRO; IPR000925;
DR INTERPRO; IPR002965;
DR PRAM; PF00802; Glycoprotein_G; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 278 AA; 30461 MW; AC113DCCDF47EDE CRC64;

Query Match      81.6%; Score 40; DB 14; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.3e-36;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KPNNDHFEVFNPCSCSNNPTCWAICKRIPNKKPGK 49
    |||||
Db 139 KPNNDHFEVFNPCSCSNNPTCWAICKRIPNKKPGK 178

RESULT 12
Q906T7 ID Q906T7 PRELIMINARY; PRT; 278 AA.
AC Q906T7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE GLYCOPROTEIN (FRAGMENT).
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=92308;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroup A and B respiratory syncytial viruses isolated over nine
RT consecutive epidemics.";
RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF193309; AAF23732.1;
DR INTERPRO; IPR000255;

Query Match      81.6%; Score 40; DB 14; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.3e-36;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KPNNDHFEVFNPCSCSNNPTCWAICKRIPNKKPGK 49
    |||||
Db 139 KPNNDHFEVFNPCSCSNNPTCWAICKRIPNKKPGK 178

RESULT 13
Q906T4 ID Q906T4 PRELIMINARY; PRT; 278 AA.
AC Q906T4
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE GLYCOPROTEIN (FRAGMENT).
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=92528;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroup A and B respiratory syncytial viruses isolated over nine
RT consecutive epidemics.";
RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF193312; AAF23735.1;
DR INTERPRO; IPR000255;
DR INTERPRO; IPR000925;
DR INTERPRO; IPR002965;
DR PRAM; PF00802; Glycoprotein_G; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 278 AA; 30474 MW; 2E05963863BF8A75 CRC64;

Query Match      81.6%; Score 40; DB 14; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.3e-36;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KPNNDHFEVFNPCSCSNNPTCWAICKRIPNKKPGK 49
    |||||
Db 139 KPNNDHFEVFNPCSCSNNPTCWAICKRIPNKKPGK 178

RESULT 14
Q906T3 ID Q906T3 PRELIMINARY; PRT; 278 AA.
AC Q906T3
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE GLYCOPROTEIN (FRAGMENT).
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
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RP SEQUENCE FROM N.A.
RC STRAIN-93006;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroup A and B respiratory syncytial viruses isolated over nine
RT consecutive epidemics.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF193313; AAF23736.1; -.
DR INTERPRO; IPR000255; -.
DR INTERPRO; IPR000925; -.
DR INTERPRO; IPR002965; -.
DR PFAM; PF00802; Glycoprotein_G; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 278 AA; 30443 MW; 8E2974F2E1AE15C9 CRC64;

Query Match 81.6%; Score 40; DB 14; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.3e-36;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KPNDFHEVFVPCISCSNNPTCWAICKRIPNKKPGKK 49
DB 139 KPNDFHEVFVPCISCSNNPTCWAICKRIPNKKPGKK 178

RESULT 15
Q906T1 PRELIMINARY; PRT; 278 AA.
ID Q906T1
AC Q906T1;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE GLYCOPROTEIN (FRAGMENT).
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-94118;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroup A and B respiratory syncytial viruses isolated over nine
RT consecutive epidemics.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF193315; AAF23738.1; -.
DR INTERPRO; IPR000255; -.
DR INTERPRO; IPR000925; -.
DR INTERPRO; IPR002965; -.
DR PFAM; PF00802; Glycoprotein_G; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 278 AA; 30481 MW; 86F307049A641648 CRC64;

Query Match 81.6%; Score 40; DB 14; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.3e-36;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KPNDFHEVFVPCISCSNNPTCWAICKRIPNKKPGKK 49
DB 139 KPNDFHEVFVPCISCSNNPTCWAICKRIPNKKPGKK 178
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Search completed: May 21, 2001, 14:19:31
Job time: 99 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 21, 2001, 14:14:51 ; Search time 18.63 Seconds
(without alignments)
150.349 Million cell updates/sec

Title: US-09-202-035-1

Perfect score: 288

Sequence: 1 KORQKPPSPKNNDFHFVF.....NNPTCWAICKRIPNKKPKRK 49

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0401.*

1: /SID56/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID56/gcgdata/geneseq/geneseq/AA1981.DAT.*
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15: /SID56/gcgdata/geneseq/geneseq/AA1994.DAT.*
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17: /SID56/gcgdata/geneseq/geneseq/AA1996.DAT.*
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22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	288	100.0	49	19 W39217	Human RSV A subtyp
2	288	100.0	49	19 W39244	Human RSV G protei
3	288	100.0	49	19 W39248	Human RSV G protei
4	288	100.0	49	19 W39250	Human RSV G protei
5	288	100.0	49	19 W39251	Human RSV G protei
6	288	100.0	298	8 P70875	Sequence of human
7	288	100.0	298	13 R25302	HSRV glycoprotein
8	288	100.0	298	19 W47005	HSRV glycoprotein
9	288	100.0	681	10 P90441	Chimeric human res
10	285	99.0	49	19 W39218	Human RSV A subtyp
11	285	99.0	49	19 W39219	Human RSV A subtyp

12	285	99.0	49	19 W39221	Human RSV A subtyp
13	285	99.0	49	19 W39222	Human RSV A subtyp
14	285	99.0	49	19 W39223	Human RSV A subtyp
15	285	99.0	49	19 W39224	Human RSV A subtyp
16	285	99.0	59	17 R97073	Respiratory Syncyt
17	285	99.0	59	20 Y44100	RSV G protein anti
18	285	99.0	61	17 R97072	Respiratory Syncyt
19	285	99.0	61	20 Y44099	RSV G protein anti
20	285	99.0	101	16 R88253	RSV sub-group A wi
21	285	99.0	101	17 R95610	RSV sub-group A wi
22	285	99.0	101	17 R95616	Respiratory Syncyt
23	285	99.0	101	17 R97050	RSV G protein anti
24	285	99.0	101	20 Y44078	A G2Na peptide der
25	285	99.0	101	21 B18805	Secreted G protein
26	285	99.0	232	20 W96314	Respiratory syncyt
27	285	99.0	298	14 R39286	Membrane bound G p
28	285	99.0	298	20 W96313	Streptococcal prot
29	285	99.0	349	17 R95660	Human RSV A subtyp
30	283	98.3	49	19 W39220	Respiratory Syncyt
31	280	97.2	57	17 R97074	RSV G protein anti
32	280	97.2	57	20 Y44101	Peptide which indu
33	270	93.8	101	20 W97311	Respiratory Syncyt
34	269	93.4	55	17 R97075	RSV G protein anti
35	269	93.4	55	20 Y44102	Peptide which indu
36	267	92.7	101	20 W97310	Respiratory Syncyt
37	265	92.0	59	17 R97080	RSV G protein anti
38	265	92.0	59	20 Y44107	Respiratory Syncyt
39	265	92.0	61	17 R97079	Respiratory Syncyt
40	265	92.0	61	20 Y44106	RSV sub-group A mod
41	265	92.0	101	16 R88255	RSV sub-group A mu
42	265	92.0	101	17 R95612	Respiratory Syncyt
43	265	92.0	101	17 R95618	Respiratory Syncyt
44	265	92.0	101	17 R97052	RSV G protein anti
45	265	92.0	101	20 Y44080	RSV G protein anti

ALIGNMENTS

RESULT 1

W39217 ID W39217 standard; peptide; 49 AA.

XX AC W39217;

XX AC W39217;

XX DT 27-AUG-1998 (first entry)

XX DE Human RSV A subtype G protein fragment (aa. 149-157) strain A2.

XX KW G protein; treatment; prevention; diagnosis; infection; immunity; antibody; Pneumovirus; identification; vaccine; cell receptor.

XX OS Human respiratory syncytial virus.

XX FH Key Location/Qualifiers

FT Disulfide-bond 25..38

FT Disulfide-bond 28..34

XX PN W09746581-A1.

XX PD 11-DEC-1997.

XX PF 04-JUN-1997; 97WO-AU00351.

XX PR 05-JUN-1996; 96AU-0000265.

XX PA (BIOM-) BIOMOLECULAR RES INST LTD.

XX PI Gorman JJ;

XX DR WPI; 1998-042117/04.

XX PT Peptide(s) derived from specific region of respiratory syncytial

PT virus G protein - used to treat, prevent, diagnose and immunise
 PT against Pneumovirus infection
 XX
 XX Claim 5; Fig 2; 75pp; English.
 PS
 CC W39217-W39234 are fragments of the human respiratory syncytial virus
 CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments
 CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
 CC infection and to immunise against such infections. Antibodies raised
 CC from these fragments may also be used diagnostically. The fragments may
 CC also be used to identify compounds able to inhibit binding of RSV to host
 CC cells and for characterisation of cell receptors for Pneumoviruses. When
 CC the fragments are used in combination with existing vaccines, they may
 CC allow a reduction in dose, and thus side effects, of the vaccine.
 XX
 XX Sequence 49 AA;
 SQ

Query Match 100.0%; Score 288; DB 19; Length 49;
 Best Local Similarity 100.0%; Pred. No. 9.2e-29;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNNDHFVFVPCISCSNPTCWAICKRIPNKKPGKK 49
 |||||
 DB 1 kqrqkppskpnndhfefvfnfpcisnptcwaickripnkpgkk 49

RESULT 2
 W39244
 ID W39244 standard; peptide; 49 AA.
 AC W39244;
 XX
 XX 27-AUG-1998 (first entry)
 DT
 XX Human RSV G protein fragment (aa. 149-157) derivative #1.
 DE
 XX G protein; treatment; prevention; diagnosis; infection; immunity;
 KW antibody; Pneumovirus; identification; vaccine; cell receptor.
 XX
 XX Human respiratory syncytial virus.
 OS
 XX
 XX Key Location/Qualifiers
 FH Modified-site 1
 FT /note= "N-terminal acetylated"
 FT Disulfide-bond 25..38
 FT Disulfide-bond 28..34
 FT Modified-site 49
 FT /note= "C-terminal amide"
 FT
 XX WO9746581-A1.
 PN
 XX 11-DEC-1997.
 PD
 XX 04-JUN-1997; 97WO-AU00351.
 PF
 XX 05-JUN-1996; 96AU-0000265.
 PR
 XX (BIOM-) BIOMOLECULAR RES INST LTD.
 PA
 XX Gorman JJ;
 PI
 XX WPI; 1998-042117/04.
 DR
 XX Peptide(s) derived from specific region of respiratory syncytial
 PT virus G protein - used to treat, prevent, diagnose and immunise
 PT against Pneumovirus infection
 XX
 XX Example 4; Fig 12; 75pp; English.
 PS
 XX W39244-W39252 are derivatives of the human respiratory syncytial virus
 CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments
 CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,

CC infection and to immunise against such infections. Antibodies raised
 CC from these fragments may also be used diagnostically. The fragments may
 CC also be used to identify compounds able to inhibit binding of RSV to host
 CC cells and for characterisation of cell receptors for Pneumoviruses. When
 CC the fragments are used in combination with existing vaccines, they may
 CC allow a reduction in dose, and thus side effects, of the vaccine.
 XX
 XX Sequence 49 AA;
 SQ

Query Match 100.0%; Score 288; DB 19; Length 49;
 Best Local Similarity 100.0%; Pred. No. 9.2e-29;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNNDHFVFVPCISCSNPTCWAICKRIPNKKPGKK 49
 |||||
 DB 1 kqrqkppskpnndhfefvfnfpcisnptcwaickripnkpgkk 49

RESULT 3
 W39248
 ID W39248 standard; peptide; 49 AA.
 AC W39248;
 XX
 XX 27-AUG-1998 (first entry)
 DT
 XX Human RSV G protein fragment (aa. 149-157) derivative #5.
 DE
 XX G protein; treatment; prevention; diagnosis; infection; immunity;
 KW antibody; Pneumovirus; identification; vaccine; cell receptor.
 XX
 XX Human respiratory syncytial virus.
 OS
 XX
 XX Key Location/Qualifiers
 FH Modified-site 1
 FT /note= "N-terminal fitc group"
 FT Disulfide-bond 25..38
 FT Disulfide-bond 28..34
 FT Modified-site 49
 FT /note= "C-terminal amide"
 FT
 XX WO9746581-A1.
 PN
 XX 11-DEC-1997.
 PD
 XX 04-JUN-1997; 97WO-AU00351.
 PF
 XX 05-JUN-1996; 96AU-0000265.
 PR
 XX (BIOM-) BIOMOLECULAR RES INST LTD.
 PA
 XX Gorman JJ;
 PI
 XX WPI; 1998-042117/04.
 DR
 XX Peptide(s) derived from specific region of respiratory syncytial
 PT virus G protein - used to treat, prevent, diagnose and immunise
 PT against Pneumovirus infection
 XX
 XX Example 4; Fig 12; 75pp; English.
 PS
 XX W39244-W39252 are derivatives of the human respiratory syncytial virus
 CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments
 CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
 CC infection and to immunise against such infections. Antibodies raised
 CC from these fragments may also be used diagnostically. The fragments may
 CC also be used to identify compounds able to inhibit binding of RSV to host
 CC cells and for characterisation of cell receptors for Pneumoviruses. When
 CC the fragments are used in combination with existing vaccines, they may
 CC allow a reduction in dose, and thus side effects, of the vaccine.
 XX
 XX Sequence 49 AA;

Query Match 100.0%; Score 288; DB 19; Length 49;
 Best Local Similarity 100.0%; Pred. No. 9.2e-29;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KORQKPPSKPNDHFVFNFCSCSNPTCWAICKRIPNKKPGKK 49
 |||
 Db 1 kqrqkppskpndhfefvfnfpcscsnptcwaickripnkkpgkk 49

RESULT 4
 W39250
 ID W39250 standard; peptide; 49 AA.
 AC W39250;
 XX
 XX 27-AUG-1998 (first entry)
 DE Human RSV G protein fragment (aa. 149-157) derivative #7.
 XX
 XX G protein; treatment; prevention; diagnosis; infection; immunity;
 KW antibody; Pneumovirus; identification; vaccine; cell receptor.
 KW
 XX Human respiratory syncytial virus.
 OS
 XX

XX Key Location/Qualifiers
 XX Modified-site 1 /note= "N-terminal bb group"
 FT Disulfide-bond 25..38
 FT Disulfide-bond 28..34
 FT Modified-site 49
 FT /note= "C-terminal amide"
 XX
 XX W09746581-A1.
 PN
 XX 11-DEC-1997.
 PD
 XX 04-JUN-1997; 97WO-AU00351.
 PF
 XX 05-JUN-1996; 96AU-0000265.
 PR
 XX (BIOM-) BIOMOLECULAR RES INST LTD.
 PA
 XX Gorman JJ;
 PI
 XX WPI; 1998-042117/04.
 DR
 XX

XX Peptide(s) derived from specific region of respiratory syncytial
 PT virus G protein - used to treat, prevent, diagnose and immunise
 PT against Pneumovirus infection
 PT
 XX

PS Example 4; Fig 12; 75pp; English.

XX W39244-W39252 are derivatives of the human respiratory syncytial virus
 CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments
 CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
 CC infection and to immunise against such infections. Antibodies raised
 CC from these fragments may also be used diagnostically. The fragments may
 CC also be used to identify compounds able to inhibit binding of RSV to host
 CC cells and for characterisation of cell receptors for Pneumoviruses. When
 CC the fragments are used in combination with existing vaccines, they may
 CC allow a reduction in dose, and thus side effects, of the vaccine.
 CC
 XX Sequence 49 AA;

Qy 1 KORQKPPSKPNDHFVFNFCSCSNPTCWAICKRIPNKKPGKK 49
 |||

Query Match 100.0%; Score 288; DB 19; Length 49;
 Best Local Similarity 100.0%; Pred. No. 9.2e-29;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KORQKPPSKPNDHFVFNFCSCSNPTCWAICKRIPNKKPGKK 49
 |||

Db 1 kqrqkppskpndhfefvfnfpcscsnptcwaickripnkkpgkk 49

RESULT 5
 W39251
 ID W39251 standard; peptide; 49 AA.
 AC W39251;
 XX
 XX 27-AUG-1998 (first entry)
 DE Human RSV G protein fragment (aa. 149-157) derivative #8.

XX G protein; treatment; prevention; diagnosis; infection; immunity;
 KW antibody; Pneumovirus; identification; vaccine; cell receptor.
 KW
 XX Human respiratory syncytial virus.
 OS
 XX

XX Key Location/Qualifiers
 XX Modified-site 1 /note= "N-terminal blot group"
 FT Disulfide-bond 25..38
 FT Disulfide-bond 28..34
 FT Modified-site 49
 FT /note= "C-terminal amide"
 XX
 XX W09746581-A1.
 PN
 XX 11-DEC-1997.
 PD
 XX 04-JUN-1997; 97WO-AU00351.
 PF
 XX 05-JUN-1996; 96AU-0000265.
 PR
 XX (BIOM-) BIOMOLECULAR RES INST LTD.
 PA
 XX Gorman JJ;
 PI
 XX WPI; 1998-042117/04.
 DR
 XX

XX Peptide(s) derived from specific region of respiratory syncytial
 PT virus G protein - used to treat, prevent, diagnose and immunise
 PT against Pneumovirus infection
 PT
 XX

PS Example 4; Fig 12; 75pp; English.

XX W39244-W39252 are derivatives of the human respiratory syncytial virus
 CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments
 CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
 CC infection and to immunise against such infections. Antibodies raised
 CC from these fragments may also be used diagnostically. The fragments may
 CC also be used to identify compounds able to inhibit binding of RSV to host
 CC cells and for characterisation of cell receptors for Pneumoviruses. When
 CC the fragments are used in combination with existing vaccines, they may
 CC allow a reduction in dose, and thus side effects, of the vaccine.
 CC
 XX Sequence 49 AA;

Qy 1 KORQKPPSKPNDHFVFNFCSCSNPTCWAICKRIPNKKPGKK 49
 |||

Query Match 100.0%; Score 288; DB 19; Length 49;
 Best Local Similarity 100.0%; Pred. No. 9.2e-29;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KORQKPPSKPNDHFVFNFCSCSNPTCWAICKRIPNKKPGKK 49
 |||
 Db 1 kqrqkppskpndhfefvfnfpcscsnptcwaickripnkkpgkk 49

RESULT 6

W39245
 ID W39245 standard; protein; 298 AA.
 XX
 AC P70845;

XX 05-APR-1991 (first entry)
 XX Sequence of human respiratory syncytial virus (HRSV) A2 strain
 DE G protein.
 DE XX
 KW Vaccine.
 XX
 OS Human respiratory syncytial virus (HRSV).
 XX
 PN W08704185-A.
 XX
 PD 16-JUL-1987.
 XX
 XX 23-DEC-1986; 86WO-US02756.
 PF
 XX 14-JAN-1986; 86US-0818740.
 PR
 XX (UYN-) UNIV OF N CAROLINA.
 PA (WERTZ) WERTZ G W.
 PA (WERTZ) WERTZ G W.
 XX
 XX WPI; 1987-206300/29.
 DR N-PSDB; N70784.
 XX
 XX Vaccines for human respiratory virus - comprising proteins or
 PT fragment encoded by a DNA sequence coding for human respiratory
 PT syncytial virus proteins.
 XX
 PS Disclosure; Chart 13; 57pp; English.
 XX
 CC A novel plasmid which comprises a DNA sequence encoding this
 CC protein, and the protein itself, are claimed, for use as HRSV
 CC vaccines. The vaccine can be administered to pregnant women or to
 CC women of child bearing age to stimulate maternal antibodies.
 CC Infants can also be vaccinated at 2-3 months of age.
 XX
 SQ Sequence 298 AA;

Query Match 100.0%; Score 288; DB 8; Length 298;
 Best Local Similarity 100.0%; Pred. No. 5.7e-28;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KORQKPPSKPNNDHFVFNVPSCISCSNPTCWAICKRIPNKKPGKK 49
 |||||
 Db 149 kqrqkppskpnndhfefvfnvpscisnptcwaickripnkkpgkk 197
 |||||

RESULT 7
 R25302
 ID R25302 standard; Protein; 298 AA.
 XX
 AC R25302;
 XX
 DT 03-MAR-1993 (first entry)
 XX
 DE HRSV glycoprotein G (gpG).
 XX
 KW Vaccine; human respiratory syncytial virus; HRSV; F; G; 22K; 9.5K;
 KW major capsid protein; N.
 XX
 OS Human respiratory syncytial virus strain A2.
 XX
 PN US5149650-A.
 XX
 PD 22-SEP-1992.
 XX
 XX 14-JAN-1986; 86US-0818740.
 PF
 XX 14-JAN-1986; 86US-0818740.
 PR
 XX 13-JUL-1988; 88US-0218737.
 XX

PA (UYN-) UNIV NORTH CAROLINA.
 XX
 PI Collins PL, Wertz GW;
 XX
 DR WPI; 1992-340247/41.
 DR N-PSDB; Q29623.
 XX
 XX Vaccines for human respiratory virus - include structural genes
 PT coding for native structural viral proteins and immunogenic
 PT fragments
 XX
 PS Disclosure; Page 18; 21pp; English.
 XX
 CC The sequences of mRNA encoding HRSV structural proteins are given in
 CC Q29622-26. The proteins are F, G, 22K, 9.5K and major capsid
 CC protein N. The sequences and encoded proteins are useful for
 CC preparing vaccines against HRSV. The vaccines can be used to confer
 CC immunity against respiratory tract infections on human subjects.
 XX
 SQ Sequence 298 AA;

Query Match 100.0%; Score 288; DB 13; Length 298;
 Best Local Similarity 100.0%; Pred. No. 5.7e-28;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KORQKPPSKPNNDHFVFNVPSCISCSNPTCWAICKRIPNKKPGKK 49
 |||||
 Db 149 kqrqkppskpnndhfefvfnvpscisnptcwaickripnkkpgkk 197
 |||||

RESULT 8
 W47605
 ID W47605 standard; Protein; 298 AA.
 XX
 AC W47605;
 XX
 DT 11-JUN-1998 (first entry)
 XX
 DE HRSV glycoprotein G.
 XX
 KW HRSV; glycoprotein F; gpF; glycoprotein G; gpG; vaccine.
 XX
 OS Human respiratory syncytial virus.
 XX
 PN US5716823-A.
 XX
 PD 10-FEB-1998.
 XX
 PF 12-MAY-1997; 97US-0854783.
 XX
 PR 13-JUL-1988; 88US-0218737.
 PR 14-JAN-1986; 86US-0818740.
 PR 23-DEC-1986; 86WO-US02756.
 PR 11-JUN-1992; 92US-0897171.
 PR 12-MAY-1997; 97US-0854783.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Collins PL, Wertz GW;
 XX
 DR WPI; 1998-144802/13.
 DR N-PSDB; V18736.
 XX
 XX Production of human respiratory syncytial virus glyco-protein F or G
 PT - by culturing eukaryotic host cells transfected with corresponding
 PT DNA
 XX
 PS Example 1; Columns 27-28; 17pp; English.
 XX
 CC The present sequence was used in the development of a novel method
 CC for the production of human respiratory syncytial virus (HRSV)
 CC glycoprotein F (gpF) or glycoprotein G (gpG). The method comprises

CC culturing eukaryotic host cells transfected with an isolated DNA
 CC sequence encoding HRSV gpF or gpG. The gp can be used to prepare
 CC vaccines against HRSV.

XX Sequence 298 AA;

Query Match 100.0%; Score 288; DB 19; Length 298;
 Best Local Similarity 100.0%; Pred. No. 5.7e-28;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKNNDFHFEVFNFCSCSNNPTCWAICKRIPNKKPGKK 49
 |||||
 Db 149 kqrqkppskpndfhfevfncscsnnptcwaickripnkkpgkk 197

RESULT 9

P90441

ID P90441 standard; protein; 681 AA.

XX AC P90441;

XX DT 01-NOV-1989 (first entry)

XX DE Chimeric human respiratory syncytial virus glycoproteins F and G.

XX KW Chimeric polypeptide; human respiratory syncytial virus;

XX KW protein F; protein G; vaccine.

XX OS Human respiratory syncytial virus.

XX PN WO8905823-A.

XX PD 29-JUN-1989.

XX PF 31-OCT-1988; 88WO-US03784.

XX PR 23-DEC-1987; 87US-0137387.

XX PA (UPJO) UPJOHN CO.

XX PI Wathen M;

XX DR WPI; 1989-206593/28.

XX PT Chimeric human respiratory syncytial virus polypeptides(s)

XX PT - contg. immunogenic fragments from HRSV glycoproteins

XX PT F and G, for vaccine prodn.

XX PS Claim 3; page 47-48; 50pp; English.

XX CC Chimeric polypeptide contg. a signal sequence and one or more

XX CC immunogenic fragments from both human respiratory syncytial virus

XX CC glycoproteins F and G. Can be used in vaccines. Hosts are, eg

XX CC E. coli, Chinese hamster ovary cells, murine C127 cells and

XX CC S. frugiperda.

XX SQ Sequence 681 AA;

Query Match 100.0%; Score 288; DB 10; Length 681;
 Best Local Similarity 100.0%; Pred. No. 1.3e-27;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKNNDFHFEVFNFCSCSNNPTCWAICKRIPNKKPGKK 49
 |||||
 Db 543 kqrqkppskpndfhfevfncscsnnptcwaickripnkkpgkk 591

RESULT 10

W39218

ID W39218 standard; peptide; 49 AA.

XX

AC W39218;

XX DT 27-AUG-1998 (first entry)

XX DE Human RSV A subtype G protein fragment (aa 149-157) strain long A.

XX KW G protein; treatment; prevention; diagnosis; infection; immunity;

XX KW antibody; Pneumovirus; identification; vaccine; cell receptor.

XX OS Human respiratory syncytial virus.

XX FH Key Location/Qualifiers

FT Disulfide-bond 25..38

FT Disulfide-bond 28..34

XX PN WO9746581-A1.

XX PD 11-DEC-1997.

XX PF 04-JUN-1997; 97WO-AU00351.

XX PR 05-JUN-1996; 96AU-0000265.

XX PA (BIOM-) BIOMOLECULAR RES INST LTD.

XX PI Gorman JJ;

XX DR WPI; 1998-042117/04.

XX PT Peptide(s) derived from specific region of respiratory syncytial

XX PT virus G protein - used to treat, prevent, diagnose and immunise

XX PT against Pneumovirus infection

XX PS Claim 5; Fig 2; 75pp; English.

XX CC W39217-W39234 are fragments of the human respiratory syncytial virus

XX CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments

XX CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,

XX CC infection and to immunise against such infections. Antibodies raised

XX CC from these fragments may also be used diagnostically. The fragments may

XX CC also be used to identify compounds able to inhibit binding of RSV to host

XX CC cells and for characterisation of cell receptors for Pneumoviruses. When

XX CC the fragments are used in combination with existing vaccines, they may

XX CC allow a reduction in dose, and thus side effects, of the vaccine.

XX SQ Sequence 49 AA;

Query Match 99.0%; Score 285; DB 19; Length 49;
 Best Local Similarity 98.0%; Pred. No. 2.2e-28;
 Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKNNDFHFEVFNFCSCSNNPTCWAICKRIPNKKPGKK 49
 |||||

Db 1 kqrqkppskpndfhfevfncscsnnptcwaickripnkkpgkk 49

RESULT 11

W39219

ID W39219 standard; peptide; 49 AA.

XX AC W39219;

XX DT 27-AUG-1998 (first entry)

XX DE Human RSV A subtype G protein fragment (aa. 149-157) strain A642.

XX KW G protein; treatment; prevention; diagnosis; infection; immunity;

XX KW antibody; Pneumovirus; identification; vaccine; cell receptor.

XX OS Human respiratory syncytial virus.

XX FH Key Location/Qualifiers

CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments
CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
CC infection and to immunise against such infections. Antibodies raised
CC from these fragments may also be used diagnostically. The fragments may
CC also be used to identify compounds able to inhibit binding of RSV to host
CC cells and for characterisation of cell receptors for Pneumoviruses. When
CC the fragments are used in combination with existing vaccines, they may
CC allow a reduction in dose, and thus side effects, of the vaccine.
XX
SQ Sequence 49 AA;

Query Match 99.0%; Score 285; DB 19; Length 49;
Best Local Similarity 98.0%; Pred. No. 2.2e-28;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORONKPSKPNNDHFVEVFNFPVCSICSNPTCWAICKRIPNKKPGKK 49
Db 1 kqrqkpnkpnndhfvevfnfvpvcsicsnnptcwaickripnkkpgkk 49

RESULT 14
W39223
ID W39223 standard; peptide; 49 AA.
XX
AC W39223;
XX
DT 27-AUG-1998 (first entry)
XX
DE Human RSV A subtype G protein fragment (aa. 149-157) strain A5857.
XX
KW G protein; treatment; prevention; diagnosis; infection; immunity;
KW antibody; Pneumovirus; identification; vaccine; cell receptor.
XX
OS Human respiratory syncytial virus.
XX

Key Location/Qualifiers
FH Disulfide-bond 25..38
FT Disulfide-bond 28..34
XX
XX WO9746581-A1.

XX 11-DEC-1997.
XX 04-JUN-1997; 97WO-AU00351.
XX 05-JUN-1996; 96AU-0000265.
XX

XX (BIOM-) BIOMOLECULAR RES INST LTD.
XX
XX Gorman JJ;
XX

XX WPI; 1998-042117/04.

XX Peptide(s) derived from specific region of respiratory syncytial
PT virus G protein - used to treat, prevent, diagnose and immunise
PT against Pneumovirus infection
XX

XX Claim 5; Fig 2; 75pp; English.

XX W39217-W39234 are fragments of the human respiratory syncytial virus
XX (RSV) G protein corresponding to amino acids 149 to 197. These fragments
XX can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
XX infection and to immunise against such infections. Antibodies raised
XX from these fragments may also be used diagnostically. The fragments may
XX also be used to identify compounds able to inhibit binding of RSV to host
XX cells and for characterisation of cell receptors for Pneumoviruses. When
XX the fragments are used in combination with existing vaccines, they may
XX allow a reduction in dose, and thus side effects, of the vaccine.
XX

XX Sequence 49 AA;

Query Match 99.0%; Score 285; DB 19; Length 49;
Best Local Similarity 98.0%; Pred. No. 2.2e-28;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORONKPSKPNNDHFVEVFNFPVCSICSNPTCWAICKRIPNKKPGKK 49
Db 1 kqrqkpnkpnndhfvevfnfvpvcsicsnnptcwaickripnkkpgkk 49

RESULT 15
W39224
ID W39224 standard; peptide; 49 AA.
XX
AC W39224;
XX
DT 27-AUG-1998 (first entry)
XX
DE Human RSV A subtype G protein fragment (aa. 149-157) strain A1734.
XX
KW G protein; treatment; prevention; diagnosis; infection; immunity;
KW antibody; Pneumovirus; identification; vaccine; cell receptor.
XX
OS Human respiratory syncytial virus.
XX

Key Location/Qualifiers
FH Disulfide-bond 25..38
FT Disulfide-bond 28..34
XX
XX WO9746581-A1.

XX 11-DEC-1997.
XX 04-JUN-1997; 97WO-AU00351.
XX 05-JUN-1996; 96AU-0000265.
XX

XX (BIOM-) BIOMOLECULAR RES INST LTD.

XX Gorman JJ;

XX WPI; 1998-042117/04.

XX Peptide(s) derived from specific region of respiratory syncytial
PT virus G protein - used to treat, prevent, diagnose and immunise
PT against Pneumovirus infection
XX

XX Claim 5; Fig 2; 75pp; English.

XX W39217-W39234 are fragments of the human respiratory syncytial virus
XX (RSV) G protein corresponding to amino acids 149 to 197. These fragments
XX can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
XX infection and to immunise against such infections. Antibodies raised
XX from these fragments may also be used diagnostically. The fragments may
XX also be used to identify compounds able to inhibit binding of RSV to host
XX cells and for characterisation of cell receptors for Pneumoviruses. When
XX the fragments are used in combination with existing vaccines, they may
XX allow a reduction in dose, and thus side effects, of the vaccine.
XX

XX Sequence 49 AA;

Query Match 99.0%; Score 285; DB 19; Length 49;
Best Local Similarity 98.0%; Pred. No. 2.2e-28;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORONKPSKPNNDHFVEVFNFPVCSICSNPTCWAICKRIPNKKPGKK 49
Db 1 kqrqkpnkpnndhfvevfnfvpvcsicsnnptcwaickripnkkpgkr 49

Search completed: May 21, 2001, 14:15:16
Job time: 25 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 21, 2001, 14:14:51 ; Search time 11.95 Seconds
(without alignments)
78.773 Million cell updates/sec

Title: US-09-202-035-1

Perfect score: 288

Sequence: 1 KORQKPPSKPNNDHFVEF.....NNPTCWAICKRIPNKKPGKK 49

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	288	100.0	681	6	Patent No. 5194595
2	285	99.0	298	2	US-08-467-963C-8
3	285	99.0	298	2	US-08-838-189D-8
4	285	99.0	298	3	US-08-852-344D-8
5	285	99.0	298	3	US-08-344-639E-8
6	285	99.0	298	4	US-08-467-969A-8
7	285	99.0	298	4	US-08-467-961A-8
8	217	75.3	37	3	US-08-793-792-12
9	193	67.0	32	3	US-08-793-792-11
10	174	60.4	28	3	US-08-793-792-4-1
11	151	52.4	37	3	US-08-793-792-11
12	145	50.3	30	4	US-08-836-504A-6
13	138	47.9	32	3	US-08-793-792-7-1
14	129	44.8	30	4	US-08-836-504A-5
15	125	43.4	28	3	US-08-793-792-3
16	96	33.3	16	3	US-08-793-792-13
17	80	27.8	263	5	PCT-US91-08177-13
18	66	22.9	32	3	US-08-793-792-6
19	66	22.9	37	3	US-08-793-792-10
20	65	22.6	28	3	US-08-793-792-2
21	64	22.2	14	4	US-08-721-979A-9
22	64	22.2	14	4	US-08-836-501-9
23	64	22.2	17	4	US-08-721-979A-20
24	64	22.2	17	4	US-08-836-501-20
25	64	22.2	28	3	US-08-793-792-1
26	64	22.2	32	3	US-08-793-792-5
27	64	22.2	37	3	US-08-793-792-9

28	61	21.2	17	4	US-08-721-979A-19	Sequence 19, Appl
29	61	21.2	17	4	US-08-836-501-19	Sequence 19, Appl
30	54	18.8	14	4	US-08-721-979A-11	Sequence 11, Appl
31	54	18.8	14	4	US-08-836-501-11	Sequence 11, Appl
32	51	17.7	198	1	US-08-052-681-1	Sequence 1, Appl
33	50.5	17.5	115	2	US-08-540-406-8	Sequence 8, Appl
34	50.5	17.5	115	3	US-08-656-055-8	Sequence 8, Appl
35	50.5	17.5	115	4	US-08-954-668-8	Sequence 8, Appl
36	50.5	17.5	115	5	PCT-US95-13233-8	Sequence 8, Appl
37	50	17.4	1121	1	US-07-789-915A-2	Sequence 2, Appl
38	50	17.4	1121	1	US-08-005-002C-2	Sequence 2, Appl
39	50	17.4	1121	1	US-08-487-203A-2	Sequence 2, Appl
40	50	17.4	1334	6	5476657-1	Patent No. 5476657
41	50	17.4	1403	2	US-07-908-253-3	Sequence 3, Appl
42	50	17.4	1403	2	US-08-694-865-17	Sequence 17, Appl
43	50	17.4	1403	2	US-08-535-837-3	Sequence 3, Appl
44	50	17.4	1403	2	US-08-124-491-17	Sequence 17, Appl
45	49.5	17.2	1940	2	US-08-644-271-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
5194595-19
; Patent No. 5194595
; APPLICANT: WATHEN, MICHAEL W.
; TITLE OF INVENTION: CHIMERIC GLYCOPROTEINS CONTAINING
; IMMUNOGENIC SEGMENT OF THE GLYCOPROTEINS OF HUMAN RESPIRATORY
; SYNCYTIAL VIRUS
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/543,780
; FILING DATE: 31-OCT-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 137,387
; FILING DATE: 23-DEC-1987
; SEQ ID NO:19:
; LENGTH: 681
5194595-19

Query Match 100.0%; Score 288; DB 6; Length 681;
Best Local Similarity 100.0%; Pred. No. 1.3e-26;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KORQKPPSKPNNDHFVEFVPCISCSNNPTCWAICKRIPNKKPGKK 49
|||||
Db 543 KORQKPPSKPNNDHFVEFVPCISCSNNPTCWAICKRIPNKKPGKK 591
|||||

RESULT 2
US-08-467-963C-8
; Sequence 8, Application US/08467963C
; Patent No. 5968776
; GENERAL INFORMATION:
; APPLICANT: KLEIN, Michel H
; APPLICANT: DU, Run-Pan
; APPLICANT: EWASYSHYN, Mary E
; TITLE OF INVENTION: MULTIMERIC HYBRID GENE ENCODING A
; TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST
; TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

Query Match 99.0%; Score 285; DB 3; Length 298;
Best Local Similarity 98.0%; Pred. No. 1.3e-26;
Matches 48; Conservative 1; Mismatches 0; Indels

Qy	1	KQRQNKPPSKPNND	FHFEVFN	FPSCSNNPTCWAICKRIPNKKPGKK	49
		:			
Db	149	KQRQNKPPSKPNND	FHFEVFN	FPSCSNNPTCWAICKRIPNKKPGKK	197

RESULT 5
US-08-344-639E-8
; Sequence 8, Application US/08344639E
; Patent No. 6033668
; GENERAL INFORMATION:
; APPLICANT: Klein, Michel H
; APPLICANT: Du, Run-Pan
; APPLICANT: Ewasyshyn, Mary E
; TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS
; TITLE OF INVENTION: PROTECTION AGAINST PARAINFLUENZA VIRUS
; TITLE OF INVENTION: AND RESPIRATORY SYNCYTIAL VIRUS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:

```

/ ADDRESS: Jim & McInnes
/ STREET: 330 University Avenue, 6th Floor
/ CITY: Toronto
/ STATE: Ontario
/ COUNTRY: Canada
/ ZIP: M5G 1R7
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0.
/
/ Version #1.25

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/ CONNAMI APPLICATION NUMBER: US/08/344,639E
/ APPLICATION NUMBER: US/08/344,639E
/ FILING DATE: 14-NOV-1994
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/001,554
/ FILING DATE: 06-JAN-1993
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9200117.1
/ FILING DATE: 06-JAN-1992
/ CLASSIFICATION: 424
/

```

ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-391 MIS
TELECOMMUNICATION INFORMATION:

```

, TELEPHONE: (416) 595-1159
,
, TELEFAX: (416) 595-1163
,
, TELEX: 065-24567 SIMBAS
,
, INFORMATION FOR SEQ ID NO: 8:
,
, SEQUENCE CHARACTERISTICS:
,
,   LENGTH: 298 amino acids
,   TYPE: amino acid
,   STRANDNESS: single
,   TOPOLOGY: linear
,
, MOLECULE TYPE: DNA (genomic)
US-08-344-6398-8

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Query Match      99.0%; Score 285; DB 3; Length 298;
Best Local Similarity 98.0%; Pred. No. 1.3e+26;
Matches 48; Conservative 1; Mismatches 0; Indels
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QY 1 KORQNKPPNNDFHFEVNFVPCISNNPTCWAICKRIPNKKPGKK 49
 |||||:|||||
 Db 149 KORQNKPPNNDFHFEVNFVPCISNNPTCWAICKRIPNKKPGKK 197

RESULT 6
US-08-467-969A-8
Sequence 8, Application US/08467969A
Patent No. 6168786
GENERAL INFORMATION:
APPLICANT: Klein, Michel H
APPLICANT: Du, Run-Pan
APPLICANT: Emasyshyn, Mary E
TITLE OF INVENTION: Chimeric Immunogens
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, 6th Floor
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,969A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-475 MIS:bh
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
TELEX: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-467-969A-8

Query Match 99.0%; Score 285; DB 4; Length 298;
Best Local Similarity 98.0%; Pred. NO. 1.3e-26;
Matches 48; Conservative 1; Mismatches 0; Indels

QY 1 KQRQKPPSKPNNDFFHFEVFNVPSCSNNPTCWAICKRIPNKKPGKK 49
 :
 Db 149 KORQKPPNKPNNDDFFHFEVFNVPSCSNNPTCWAICKRIPNKKPGKK 197

RESULT 7
US-08-467-961A-8
: Sequence 8, Application US/08467961A
: Patent No. 6171783
: GENERAL INFORMATION:
: APPLICANT: Klein, Michael H
: APPLICANT: Du, Run-Pan
: APPLICANT: Ewasyshyn, Mary E
: TITLE OF INVENTION: Chimeric Immun
: NUMBER OF SEQUENCES: 21
: CORRESPONDENCE ADDRESS:
:

ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, 6TH Floor
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,961A
FILING DATE: 06-JUN-1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I

REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-476 MIS:bh

TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
TELEX: 065-24567 SIMBAS

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-467-961A-8

Query Match 99.0%; Score 285; DB 4; Length 298;
Best Local Similarity 98.0%; Pred. No. 1.3e-26;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORONKPPKPNNDHFEVFNPCSCSNNPTCWAICKRIPKPKGK 49
|||||
DB 149 KORONKPPKPNNDHFEVFNPCSCSNNPTCWAICKRIPKPKGK 197

RESULT 8

US-08-793-792 (12)
Sequence 12 Application US/08793792

Patent No. 6077511
GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Antigenic peptides derived from the

TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis

TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.

NUMBER OF SEQUENCES: 13

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,792

FILING DATE:

CLASSIFICATION: 514

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 37 amino acids

TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-793-792-12

Query Match 75.3%; Score 217; DB 3; Length 37;
Best Local Similarity 97.3%; Pred. No. 1.8e-19;
Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 SKPNDFHFEVFNPCSCSNNPTCWAICKRIPNKK 45
|||||
DB 1 NKPNDHFEVFNPCSCSNNPTCWAICKRIPNKK 37

RESULT 9

US-08-793-792 (8)
Sequence 8 Application US/08793792

Patent No. 6077511
GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Antigenic peptides derived from the

TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis

TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.

NUMBER OF SEQUENCES: 13

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,792

FILING DATE:

CLASSIFICATION: 514

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 32 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

US-08-793-792 (8)

Query Match 67.0%; Score 193; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 KPNDHFEVFNPCSCSNNPTCWAICKRI 32

RESULT 10

US-08-793-792 (4)
Sequence 4 Application US/08793792

Patent No. 6077511
GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Antigenic peptides derived from the

TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis

TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.

NUMBER OF SEQUENCES: 13

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,792

FILING DATE:

12-8, 4

CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-793-792-4

Query Match 60.4%, Score 174, DB 3, Length 28
Best Local Similarity 100.0%, Pred. No. 1.6e-14
Matches 28, Conservative 0, Mismatches 0, Indels 0, Gaps 0
Qy 11 PNNDFHEVFVPCISCSNNPTCAIC 38
Db 1 PNNDFHEVFVPCISCSNNPTCAIC 28

RESULT 11
US-08-793-792-11
Sequence 11, Application US/08793792
Patent No. 6077511
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Antigenic peptides derived from the
TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis
TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.
NUMBER OF SEQUENCES: 13
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION NUMBER: US/08/793.792
FILING DATE:
CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-793-792-11

Query Match 52.4%, Score 151, DB 3, Length 37;
Best Local Similarity 69.4%, Pred. No. 1.1e-11;
Matches 25; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
Qy 10 KPNDFHEVFVPCISCSNNPTCAICKIPNKK 45
Db 2 KPNDDYHEVFVPCISCGNNQLCKSICKTIPSNK 37

RESULT 12
US-08-836-504A-6
Sequence 6, Application US/08836504A
Patent No. 6130091
GENERAL INFORMATION:
APPLICANT: Binz, Hans
APPLICANT: Nguyen Ngoc, Thien
APPLICANT: Stahl, Stefan
APPLICANT: Uhlen, Mathias
APPLICANT: Nygren, Per Ake
TITLE OF INVENTION: Method for obtaining a peptide derived
TITLE OF INVENTION: from the respiratory syncytial virus, polypeptide and
TITLE OF INVENTION: bacteria expressing it, and their applications as

TITLE OF INVENTION: medicinal product.
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rocky, Milnamow & Katz
STREET: 180 N. Stetson Avenue, 2 Prudential Plaza,
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836.504A
FILING DATE: 07-MAY-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Katz, Martin L.
REGISTRATION NUMBER: 25,011
REFERENCE/DOCKET NUMBER: PIE1514P0200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-836-504A-6

Query Match 50.3%, Score 145, DB 4; Length 30;
Best Local Similarity 89.7%, Pred. No. 4.8e-11;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 21 NVPVCSISNNPTCAICKRIPNKPGRK 49
Db 1 NNPVCSISNNPTCAICKRIPNKPGRK 29

RESULT 13
US-08-793-792-7
Sequence 7, Application US/08793792
Patent No. 6077511
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Antigenic peptides derived from the
TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis
TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.
NUMBER OF SEQUENCES: 13
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793.792
FILING DATE:
CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-793-792-7

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 21, 2001, 14:14:51 ; Search time 12.88 seconds
(without alignments)
261.446 Million cell updates/sec

Title: US-09-202-035-1

Perfect score: 288

Sequence: 1 KORQNKPPSKPNDFHFEVFN.....NNPTCWAICKRIPNKKPGKK 49

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_67:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	288	100.0	298	1	MGNZ	major surface glycoprotein
2	285	99.0	297	2	JQ1205	attachment protein
3	285	99.0	297	2	JQ1204	attachment protein
4	285	99.0	297	2	JQ1208	attachment protein
5	285	99.0	298	1	MGNZRL	major surface glycoprotein
6	285	99.0	298	2	JC5680	G protein - Human
7	280	97.2	298	2	JQ1207	attachment protein
8	279	96.9	297	2	JQ1206	attachment protein
9	273	94.8	297	2	JQ1209	attachment protein
10	190	66.0	292	1	MGNZ18	major surface glycoprotein
11	190	66.0	292	1	MGNZ60	major surface glycoprotein
12	83.5	29.0	257	1	MGNZBR	major surface glycoprotein
13	80	27.8	263	2	JQ2284	glycoprotein G - b
14	79	27.4	250	2	PQ0768	glycoprotein G - b
15	77.5	26.9	248	2	PQ0769	glycoprotein G - b
16	77.5	26.9	263	2	JQ2388	glycoprotein G - o
17	77.5	26.9	263	2	A48732	attachment glycoprotein
18	66.5	23.1	275	1	S01913	diaminopimelate ep
19	64	22.2	37	2	B60963	charybdotoxin 2
20	63.5	22.0	274	2	F64090	diaminopimelate ep
21	63	21.9	1861	2	T13845	microtubule-associ
22	62	21.5	37	2	A03963	charybdotoxin 1 [v
23	62	21.5	290	2	G82360	diaminopimelate ep
24	59	20.5	57	2	S70473	neurotoxin Ts-kapp
25	58.5	20.3	276	2	G82986	diaminopimelate ep
26	57.5	20.0	276	2	T10459	diaminopimelate ep
27	57.5	20.0	518	2	T25507	hypothetical prote
28	57.5	20.0	776	2	T02584	hypothetical prote
29	57	19.8	279	2	C70458	diaminopimelate ep

hypothetical prote
gene e1 protein -
hypothetical prote
basic juvenile hor
r-cell surface gly
sex-specific stora
hypothetical prote
SYG1 protein - yea
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote

ALIGNMENTS

RESULT 1
MGNZ
Major surface glycoprotein G - human respiratory syncytial virus
C;Species: human respiratory syncytial virus
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 24-Sep-1999
C;Accession: A94048; A93599; A04039
R;Wertz, G.W.; Collins, P.L.; Huang, Y.; Gruber, C.; Levine, S.; Ball, L.A.
Proc. Natl. Acad. Sci. U.S.A. 82, 4075-4079, 1985
A;Title: Nucleotide sequence of the G protein gene of human respiratory syncytial vir
A;Reference number: A94048; MUID:85216636
A;Accession: A94048
A;Molecule type: mRNA
A;Residues: 1-298 <WER>
A;Cross-references: GB:M11486; GB:K01459; GB:K02719; GB:K03348; GB:K03349; GB:M11217;
7.1; PID:g333932
A;Note: residues 207-298 are identical with residues 376-467 of the nucleocapsid prot
R;Satake, M.; Colligan, J.E.; Elango, N.; Norrby, E.; Venkatesan, S.
Nucleic Acids Res. 13, 7795-7812, 1985
A;Title: Respiratory syncytial virus envelope glycoprotein (G) has a novel structure.
A;Reference number: A93599; MUID:86067198
A;Accession: A93599
A;Molecule type: mRNA
A;Residues: 1-298 <SAT>
A;Cross-references: GB:X03149; NID:g60997; PIDN:CAA26928.1; PID:g60998
C;Superfamily: respiratory syncytial virus major surface glycoprotein G
C;Keywords: glycoprotein; transmembrane protein
F;38-66/Domain: transmembrane #status predicted <TNN>
F;85,135,237,251/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 288; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.4e-26;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQNKPPSKPNDFHFEVFNFCSCSNPTCWAICKRIPNKKPGKK 49
|||||
Db 149 KORQNKPPSKPNDFHFEVFNFCSCSNPTCWAICKRIPNKKPGKK 197

RESULT 2
JQ1205
attachment protein - human respiratory syncytial virus (strain RSB1734)
N;Alternate names: G protein
C;Species: human respiratory syncytial virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1987
C;Accession: JQ1205
R;Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
A;Title: Identification of variable domains of the attachment (G) protein of subgroup
A;Reference number: JQ1204; MUID:91374005
A;Accession: JQ1205

RESULT 5
MGNZRL

major surface glycoprotein G - human respiratory syncytial virus
C:Species: human respiratory syncytial virus
C:date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change
C:Accession: A32703; S12279
R:Johnson, P.R.; Strickland, M.K.; Olmsted, R.A.; Collins, P.L.

Proc. Natl. Acad. Sci. U.S.A. 84, 5625-5629, 1987
A;Title: The G glycoprotein of human respiratory syncytial virus
A;Reference number: A32703; MUID:87289657
A;Accession: A32703

A: Molecule type: mRNA
A: Residues: 1-298 <TOH>
A: Cross-references: GB:M17212; NID:G33940; PTDN:AAA47411.1; P
R: Garcia-Barreno, B.; Portela, A.; Delgado, T.; Lopez, J.A.; Me
EMBO J. 9, 4181-4187, 1990

A;Title: Frame shift mutations as a novel mechanism for the
A;Reference number: S12279; WUID:91065351
A;Accession: S12279
A;Molecule type: mRNA
A;Residues: 1-298 <GAR>

C;Superfamily: respiratory syncytial virus major surface glycoprotein
C;Keywords: glycoprotein; transmembrane protein
F;F1-63/Domain: transmembrane #status predicted <TM>
F;85, 103, 135, 179, 237, 250, 251, 273, 294/Binding site: carbohydrate

Query Match 99.0%; Score 205; DB 1; Length 238
 Best Local Similarity 98.0%; Pred. No. 3.2e-26;
 Matches 48; Conservative 1; Mismatches 0; Indels

QY 1 K Q R N P P S K P N D F H E V F N F V P C S I C S N N P T C W A I C R I P N K K P G K K 49
 | | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 149 K Q R N P P P K P N D F H E V F N F V P C S I C S N N P T C W A I C R I P N K K P G K K 197

RESULT 6
JC3680
G protein - Human respiratory syncytial virus
C:Species: Human respiratory syncytial virus

C/Date: 11-Nov-1997 #sequence_revision 11-Nov-1997 #text_changed
C/Accession: J035680
R/Geng, X.; Wang, Z.; Qian, Y.; Zhu, R.; Deng, J.; Du, J.; Zhu, H.;
Chinese J. Virol. 12, 317-322, 1996
A/Title: Molecular analysis of G protein gene of a respiratory
A/rifle: Molecular analysis of G protein gene of a respiratory

A;Reference number: JC5680
A;Accession: JC5680
A;Molecule type: mRNA
A;Residues: 1-298 <GEN>
A;Experimental source: strain B79

A: Note: the authors translated the codon TTT for residue 165 as
C: Superfamily: respiratory syncytial virus major surface glycoprotein
F; 1-38/Domain: Intracellular #status predicted <INT>
F; 39-66/Domain: transmembrane #status predicted <TM>
F; 67-298/Domain: extracellular #status predicted <EXC>

Query Match 99.0%; Score 285; DB 2; Length 298
 Best Local Similarity 98.0%; Pred. No. 3.2e-26;
 Matches 48; Conservative 1; Mismatches 0; Indels 0;

QY 1 KORQKPPSKPNNDFFEEVFENFVPCISCNNTCWAICKRIPIKNKP GK 49
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 149 KORQKPPSKPNNDFFEEVFENFVPCISCNNTCWAICKRIPIKNKP GK 197

RESULT 7
JQ1207

C;Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract
er children and adults.
C;Superfamily: respiratory syncytial virus major surface glycoprotein G
C;Keywords: glycoprotein; transmembrane protein
F;85,103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covalent) #status pred
C;Accession: A37077

Query Match 94.88; Score 273; DB 2; Length 297;
Best Local Similarity 93.9%; Pred. No. 8.1e-25;
Matches 46; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KQKQKPPKPNDDFHEVFNFVPCISCSNNPTCWAICKRIPNKKPGKK 49
|| |||||:|||| |||||:|||||:|||||:|||||:|||||:|||||
DB 149 KQKQKPPKPNDDFHEVFNFVPCISCSNNPTCWAICKRIPNKKPGKK 197

RESULT 10
MGN218
major surface glycoprotein G - human respiratory syncytial virus (strain 18537)
C;Species: human respiratory syncytial virus
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
C;Accession: B32703
R;Johnson, P.R.; Spriggs, M.K.; Olmsted, R.A.; Collins, P.L.
Proc. Natl. Acad. Sci. U.S.A. 84, 5625-5629, 1987
A;Title: The G glycoprotein of human respiratory syncytial viruses of subgroups A and
A;Reference number: A32703; MUID:87289657
A;Accession: B32703
A;Molecule type: mRNA
A;Residues: 1-292 <TOH>
A;Cross-references: GB:M1713; NID:g333942; PIDN:AAA47412.1; PID:g333943
C;Superfamily: respiratory syncytial virus major surface glycoprotein G
C;Keywords: glycoprotein; transmembrane protein
F;41-63/Domain: transmembrane #status predicted <TMN>
F;81,86,100/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 56.08; Score 190; DB 1; Length 292;
Best Local Similarity 65.3%; Pred. No. 4.3e-15;
Matches 32; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 KQKQKPPKPNDDFHEVFNFVPCISCSNNPTCWAICKRIPNKKPGKK 49
|| || |||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 149 KRSKNPPKPKDDYHFEVFNFVPCISCGNNQLCKSICKTIPSNRPPKK 197

RESULT 11
MGN260
major surface glycoprotein G - human respiratory syncytial virus (strain 8/60)
N;Alternate names: attachment glycoprotein G
C;Species: human respiratory syncytial virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C;Accession: A37077
R;Sullender, W.M.; Anderson, K.; Wertz, G.W.
Virology 178, 195-203, 1990
A;Title: The respiratory syncytial virus subgroup B attachment glycoprotein: analysis
gous subgroup virus challenge.
A;Reference number: A37077; MUID:90357765
A;Accession: A37077
A;Molecule type: mRNA
A;Residues: 1-292 <SUL>
A;Cross-references: EMBL:M55633; NID:g333944; PIDN:AAA47413.1; PID:g333945
C;Genetics:
A;Gene: G
C;Superfamily: respiratory syncytial virus major surface glycoprotein G
C;Keywords: glycoprotein; transmembrane protein
F;45-63/Domain: transmembrane #status predicted <TMN>
F;81,86,100,230,290/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 66.08; Score 190; DB 1; Length 292;
Best Local Similarity 65.3%; Pred. No. 4.3e-15;
Matches 32; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: May 21, 2001, 14:15:36 ; Search time 8.11 seconds
(without alignments)
206.969 Million cell updates/sec

Title: US-09-202-035-1

Perfect score: 288

Sequence: 1 KORQNKPPSKPNDFEVE.....NNPTCWAICKRIPNKKGKK 49

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	288	100.0	298	1 VGLG_HRSVA	P03423 human respi
2	285	99.0	297	1 VGLG_HRSV2	P27021 human respi
3	285	99.0	297	1 VGLG_HRSV3	P27022 human respi
4	285	99.0	297	1 VGLG_HRSV6	P27025 human respi
5	285	99.0	298	1 VGLG_HRSV1	P20895 human respi
6	280	97.2	298	1 VGLG_HRSV5	P27024 human respi
7	279	96.9	297	1 VGLG_HRSV4	P27023 human respi
8	273	94.8	297	1 VGLG_HRSV7	P27026 human respi
9	190	66.0	292	1 VGLG_HRSV1	P20896 human respi
10	190	66.0	292	1 VGLG_HRSV8	P23041 human respi
11	83.5	29.0	257	1 VGLG_HRSVC	P22261 bovine resp
12	80	27.8	263	1 VGLG_BRSV2	O10685 bovine resp
13	77.5	26.9	257	1 VGLG_BRSV5	O10686 bovine resp
14	77.5	26.9	263	1 VGLG_BRSVW	O10687 bovine resp
15	77.5	26.9	263	1 VGLG_ORSVW	Q86695 ovine respi
16	76.5	26.6	263	1 VGLG_BRSV1	O10683 bovine respi
17	76.5	26.6	263	1 VGLG_BRSV4	O10684 bovine respi
18	74	25.7	257	1 VGLG_BRSV1	O09495 bovine respi
19	74	25.7	257	1 VGLG_BRSVR	Q84183 bovine respi
20	73	25.3	257	1 VGLG_BRSV7	Q85706 bovine respi
21	66.5	23.1	198	1 DAPF_YERPE	P46357 yersinia pe
22	66.5	23.1	274	1 DAPF_ECOLI	P08885 escherichia
23	64	22.2	37	1 SCK2_LEIQH	P45628 leiurus qui
24	63.5	22.0	274	1 DAPF_HAEIN	P44859 haemophilus
25	62	21.5	37	1 SCKC_LEIQH	P13487 leiurus qui
26	58.5	20.3	276	1 DAPF_PSEAE	Q51584 pseudomonas
27	57.5	20.0	276	1 DAPF_PSEAE	O05322 pseudomonas
28	57	19.8	279	1 DAPF_AFLQ	O67693 aquifex aeo
29	56.5	19.6	748	1 JSB1_TRINI	Q06342 trichoplusi
30	55.5	19.3	747	1 SSPI_BOMMO	P09179 bombyx mori
31	55	19.1	35	1 SCKK_TITSE	P56219 tityx serr
32	54.5	18.9	902	1 SYGI_YEAST	P40528 saccharomyc
33	54	18.8	160	1 LSPA_BUCAI	P57248 buchnera ap

RESULT	1	VGLG_HRSVA	STANDARD;	PRT;	298 AA.
34	53.5	18.6	237	1	HK31_MOUSE
35	52.5	18.2	284	1	DAPE_BUCAI
36	52.5	18.2	360	1	MTSB_LALCI
37	52	18.1	102	1	VE7_PAPVE
38	52	18.1	454	1	TNRI_MOUSE
39	52	18.1	2386	1	RAD3_SCHPO
40	51.5	17.9	354	1	MBHS_WOLSH
41	51	17.7	36	1	SCK3_LEIQH
42	51	17.7	118	1	YK07_YEAST
43	51	17.7	245	1	YIT8_YEAST
44	51	17.7	675	1	PRTS_MOUSE
45	51	17.7	1059	1	CERU_RAT

ALIGNMENTS

P97436 mus musculu
P57649 buchnera ap
P34878 lactococcus
P11332 european el
P25118 mus musculu
Q02039 schizosacch
P31884 wolliella s
P45660 leiurus qui
P32858 saccharomyc
P40574 saccharomyc
C08761 mus musculu
P13635 rattus norv

Human respiratory syncytial virus (strain A2).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11259;
SEQUENCE FROM N.A.
MEDLINE=85216636; PubMed=3858865;
Wertz G.W., Collins P.L., Huang Y., Gruber C., Levine S., Ball L.A.;
"Nucleotide sequence of the G protein gene of human respiratory
syncytial virus reveals an unusual type of viral membrane protein.";
Proc. Natl. Acad. Sci. U.S.A. 82:4075-4079(1985).
[2]
SEQUENCE FROM N.A.
MEDLINE=86067198; PubMed=4069997;
Satake M., Colligan J.E., Elango N., Norrby E., Venkatesan S.;
"Respiratory syncytial virus envelope glycoprotein (G) has a novel
structure.";
Nucleic Acids Res. 13:7795-7812(1985).
[3]
SEQUENCE FROM N.A.
MEDLINE=95266253; PubMed=7747420;
Connors M., Crowe J.E. Jr., Firestone C.Y., Murphy B.R., Collins P.L.;
"A cold-passaged, attenuated strain of human respiratory syncytial
virus contains mutations in the F and L genes.";
Virology 208:478-484(1995).
[4]
SEQUENCE FROM N.A.
MEDLINE=97187925; PubMed=9035372;
Crowe J.E. Jr., Firestone C.Y., Whitehead S.S., Collins P.L.,
Murphy B.R.;
"Acquisition of the ts phenotype by a chemically mutagenized cold-
passaged human respiratory syncytial virus vaccine candidate results
from the acquisition of a single mutation in the polymerase (L)
gene.";
Virus Genes 13:269-273(1996).
-|- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
HEMAGGLUTININATING ACTIVITIES.
-|- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
-|- PFM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.

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 CC or send an email to license@isb-sib.ch).

DR EMBL: M11486; AAB59857.1; -
 DR EMBL: X03149; CAA26928.1; -
 DR EMBL: U50362; AAB86663.1; -
 DR EMBL: U50363; AAB86675.1; -
 DR EMBL: U63644; AAC55969.1; -
 DR PIR: A04039; MGZ.
 DR InterPro: IPR000925; -
 DR Pfam: PF00802; Glycoprotein_G; 1.
 KW Transmembrane; Glycoprotein.
 FT DOMAIN 1 37
 FT TRANSMEM 38 66
 FT DOMAIN 67 298
 FT CARBOHYD 135 135
 FT CARBOHYD 237 237
 FT CARBOHYD 251 251
 FT CARBOHYD 251 251
 SQ SEQUENCE 298 AA; 32586 MW; 993C3D2DD68BC634 CRC64;

Query Match 100.0%; Score 288; DB 1; Length 298;

Best Local Similarity 100.0%; Pred. No. 1.1e-26;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KORQKPPSKPNDFFHFVFPVCSICSNPTCWAICKRIPNKKPGKK 49
 DB 149 KORQKPPSKPNDFFHFVFPVCSICSNPTCWAICKRIPNKKPGKK 197

RESULT 2

ID VGLG_HRSV2 STANDARD; PRT; 297 AA.
 AC P27021;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-AUG-1992 (Rel. 23, Last annotation update)
 DE MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).
 GN G.
 OS Human respiratory syncytial virus (strain rsb642).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
 OX NCBI_TaxID=11252;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91374005; PubMed=1895054;
 RA Cane P.A., Matthews D.A., Pringle C.R.;
 RT "Identification of variable domains of the attachment (G) protein of
 RT subgroup A respiratory syncytial viruses.";
 RL J. Gen. Virol. 72:2091-2096(1991).
 CC -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
 CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
 CC HEMAGGLUTININATING ACTIVITIES.
 CC -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
 CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
 CC -1- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
 CC DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
 DR PIR: J01204; J01204.
 DR InterPro: IPR000925; -
 DR Pfam: PF00802; Glycoprotein_G; 1.
 KW Transmembrane; Glycoprotein.
 FT DOMAIN 1 37
 FT TRANSMEM 38 66
 FT DOMAIN 67 297
 FT CARBOHYD 135 135
 FT CARBOHYD 144 144
 FT CARBOHYD 237 237
 FT CARBOHYD 251 251
 SQ SEQUENCE 297 AA; 32745 MW; FC72A7F3A8EBF67C CRC64;

Query Match 99.0%; Score 285; DB 1; Length 297;
 Best Local Similarity 98.0%; Pred. No. 2.4e-26;

Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 KORQKPPSKPNDFFHFVFPVCSICSNPTCWAICKRIPNKKPGKK 49
 DB 149 KORQKPPSKPNDFFHFVFPVCSICSNPTCWAICKRIPNKKPGKR 197

RESULT 3

VGLG_HRSV3 STANDARD; PRT; 297 AA.
 AC P27022;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-AUG-1992 (Rel. 23, Last annotation update)
 DE MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).
 GN G.
 OS Human respiratory syncytial virus (strain rsb1734).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
 OX NCBI_TaxID=11253;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91374005; PubMed=1895054;
 RA Cane P.A., Matthews D.A., Pringle C.R.;
 RT "Identification of variable domains of the attachment (G) protein of
 RT subgroup A respiratory syncytial viruses.";
 RL J. Gen. Virol. 72:2091-2096(1991).
 CC -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
 CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
 CC HEMAGGLUTININATING ACTIVITIES.
 CC -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
 CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
 CC -1- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
 CC DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
 DR PIR: JQ1205; JQ1205.
 DR InterPro: IPR000925; -
 DR Pfam: PF00802; Glycoprotein_G; 1.
 KW Transmembrane; Glycoprotein.
 FT DOMAIN 1 37
 FT TRANSMEM 38 66
 FT DOMAIN 67 297
 FT CARBOHYD 135 135
 FT CARBOHYD 237 237
 FT CARBOHYD 251 251
 FT CARBOHYD 251 251
 SQ SEQUENCE 297 AA; 32525 MW; 48448F9E091E1802 CRC64;

Query Match 99.0%; Score 285; DB 1; Length 297;
 Best Local Similarity 98.0%; Pred. No. 2.4e-26;

Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KORQKPPSKPNDFFHFVFPVCSICSNPTCWAICKRIPNKKPGKK 49
 DB 149 KORQKPPSKPNDFFHFVFPVCSICSNPTCWAICKRIPNKKPGKR 197

RESULT 4

VGLG_HRSV6 STANDARD; PRT; 297 AA.
 AC P27025;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-AUG-1992 (Rel. 23, Last annotation update)
 DE MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).
 GN G.
 OS Human respiratory syncytial virus (strain rsb6256).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
 OX NCBI_TaxID=11256;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91374005; PubMed=1895054;
 RA Cane P.A., Matthews D.A., Pringle C.R.;

InterPro: IPR000925; --
Pfam: PF08002; Glycoprotein_G; 1.
DR Transmembrane; Glycoprotein.
KW
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 38 66 POTENTIAL.
FT DOMAIN 67 298 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 103 103 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 237 237 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 250 250 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 251 251 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. .) (POTENTIAL).
SEQUENCE 298 AA; 32781 MW; B79FEFA4B4A73B0E CRC64;

Query Match 99.0%; Score 285; DB 1; Length 298;
Best Local Similarity 98.0%; Pred. No. 2.4e-26;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQRKNPPSPKPNDFHFEVFNVPSCISNNPTCWAICKRIPNKKPKGK 49
|||||:|||||:|||||:|||||:|||||:|||||:
Db 149 KORKNPPKPNDFHFEVFNVPSCISNNPTCWAICKRIPNKKPKGK 197

RESULT 6
VGLG_HRSVS ID VGLG_HRSVS STANDARD; PRT; 298 AA.
AC P27024;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).
GN GN
OS Human respiratory syncytial virus (strain rsb6190).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxId=11255;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91374005; PubMed=1895054;
RW Cane P.A., Matthews D.A., Pringle C.R.:
RT "Identification of variable domains of the attachment (G) protein of
RL subgroup A respiratory syncytial viruses.";
RL J. Gen. Virol. 72:2091-2096(1991).
CC -! FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
CC HEMAGGLUTININATING ACTIVITIES.
CC -! SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
CC -! PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
CC DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
PIR; JQ1207; JQ1207.

InterPro: IPR000925; --
DR Pfam: PF08002; Glycoprotein_G; 1.
DR Transmembrane; Glycoprotein.
KW
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 38 66 POTENTIAL.
FT DOMAIN 67 298 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 103 103 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 237 237 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 250 250 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. .) (POTENTIAL).
SEQUENCE 298 AA; 32769 MW; 4D7AE854D34D7BA5 CRC64;

Query Match 97.2%; Score 280; DB 1; Length 298;
Best Local Similarity 95.9%; Pred. No. 9.1e-26;
Matches 47; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQRKNPPSPKPNDFHFEVFNVPSCISNNPTCWAICKRIPNKKPKGK 49
|||||:|||||:|||||:|||||:|||||:|||||:
Db 149 KORKNPPKPNDFHFEVFNVPSCISNNPTCWAICKRIPNKKPKGK 197

KW Transmembrane; Glycoprotein.
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 38 66 POTENTIAL.
FT DOMAIN 67 292 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 292 AA; 32306 MW; BC8C59F69CA7AFC2 CRC64;

Query Match 66.0%; Score 190; DB 1; Length 292;
Best Local Similarity 65.3%; Pred. No. 2.7e-15;
Matches 32; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

Qy 1 KQKQKPPSKPNDHFVFNFCVCSICSNPTCAICKRIPNKKPGKK 49
Db 149 KSRKNPKPKDDYHFEVFNFCVCSICGNQLCKSICKTIPSNKPKK 197

RESULT 10
VGLG_HRSV8 STANDARD; PRT; 292 AA.
AC P23041;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).
GN G.
OS Human respiratory syncytial virus (subgroup B / strain 8/60).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11258;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90357765; PubMed=1697126;
RA Sullender W.M., Anderson K., Wertz G.W.;
RT "The respiratory syncytial virus subgroup B attachment glycoprotein:
analysis of sequence, expression from a recombinant vector, and
evaluation as an immunogen against homologous and heterologous
subgroup virus challenge.";
RL Virology 178:195-203(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91374595; PubMed=1895391;
RA Sullender W.M., Mufson M.M., Anderson L.J., Wertz G.W.;
RT "Genetic diversity of the attachment protein of subgroup B
respiratory syncytial viruses.";
RL J. Virol. 65:5425-5434(1991).

CC -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
HEMAGGLUTININATING ACTIVITIES.
CC -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
CC -1- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.

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EMBL; M55633; AAA47413.1; -
DR EMBL; M73545; AAA47408.1; -
DR PIR; A37077; MGNZ60.
DR InterPro; IPR000925; -
DR Pfam; PF00802; Glycoprotein_G; 1.
KW Transmembrane; Glycoprotein.
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 38 66 POTENTIAL.
FT DOMAIN 67 292 EXTRACELLULAR (POTENTIAL).

FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 292 AA; 32143 MW; 8EC60C85EF057BB5 CRC64;

Query Match 66.0%; Score 190; DB 1; Length 292;
Best Local Similarity 65.3%; Pred. No. 2.7e-15;
Matches 32; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

Qy 1 KQKQKPPSKPNDHFVFNFCVCSICSNPTCAICKRIPNKKPGKK 49
Db 149 KSRKNPKPKDDYHFEVFNFCVCSICGNQLCKSICKTIPSNKPKK 197

RESULT 11
VGLG_BRSV8 STANDARD; PRT; 257 AA.
AC P22261;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).
GN G.

OS Bovine respiratory syncytial virus (strain Copenhagen) (BRS).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11248;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91012801; PubMed=2214024;
RA Lerch R.A., Anderson K., Wertz G.W.;
RT "Nucleotide sequence analysis and expression from recombinant vectors
demonstrate that the attachment protein G of bovine respiratory
syncytial virus is distinct from that of human respiratory syncytial
virus.";
RL J. Virol. 64:5559-5569(1990).
RN [2]
RP STRUCTURE BY NMR OF 158-189.
RC STRAIN=391-2;
RX MEDLINE=97098087; PubMed=8942628;
RA Doreleijers J.F., Langedijk J.P.M., Haard K., Boelens R.,
Rullmann J.A., Schaaper W.M., van Oirschot J.T., Kaptein R.;
RT "Solution structure of the immunodominant region of protein G of
bovine respiratory syncytial virus.";
RL Biochemistry 35:14684-14688(1996).

CC -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
HEMAGGLUTININATING ACTIVITIES.

CC -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.

CC -1- SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B
HRS VIRUS.

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EMBL; M58307; AAA42810.1; -
DR PIR; A36408; MGNZBR.
DR PDB; 1BRV; 05-JUN-97.
DR InterPro; IPR000925; -
DR Pfam; PF00802; Glycoprotein_G; 1.
KW Transmembrane; Glycoprotein; 3D-structure.
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 38 66 POTENTIAL.
FT DOMAIN 67 257 EXTRACELLULAR (POTENTIAL).
FT DISULFID 173 186
FT DISULFID 176 182

FT CARBOHYD 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 233 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 251 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 257 AA; 28569 MW; 0B86D541PBA0657D CRC64;

Query Match 29.0%; Score 83.5; DB 1; Length 257;
 Best Local Similarity 29.6%; Pred. No. 0.0061;
 Matches 16; Conservative 9; Mismatches 16; Indels 13; Gaps 2;

QY 6 KPPSKPNDF-----HFEVFNVPSCISNNPTCWAIC-----KRIPNKKP 46
 ||| | : : : |||| | | : : : ||| : : : |
 Db 145 KPPINPSSGIPENHQNDFVPCSTCEGNLACLCLSIETRAPSR 198

RESULT 12
 VGLG_BRSV2
 ID VGLG_BRSV2 STANDARD; PRT; 263 AA.

AC O10685;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).
 GN G.

OS Bovine respiratory syncytial virus (strain 220-60) (BRS).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
 OX NCBI_TaxID=82819;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=97288324; PubMed=9143302;
 RA Furze J., Roberts S., Wertz G., Taylor G.;
 RT "Antigenically distinct G glycoproteins of BRSV strains share a high
 RT degree of genetic homogeneity.";
 RL Virology 231:48-58(1997).

CC -!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
 CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
 CC HEMAGGLUTININATING ACTIVITIES.

CC -!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
 CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.

CC -!- SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B
 CC HRS VIRUS.

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DR EMBL; Y11205; CA72089.1; -.
 DR HSP; P22261; IBRV.
 DR InterPro; IPR000925; -.
 DR Pfam; PF00802; Glycoprotein_G; 1.

KW Transmembrane; Glycoprotein.
 FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 38 66 POTENTIAL.
 FT DOMAIN 67 263 EXTRACELLULAR (POTENTIAL).
 FT DISULFID 173 186 BY SIMILARITY.
 FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 263 AA; 28964 MW; A630883D51ED02D5 CRC64;

Query Match 27.8%; Score 80; DB 1; Length 263;
 Best Local Similarity 29.8%; Pred. No. 0.016;
 Matches 14; Conservative 9; Mismatches 20; Indels 4; Gaps 1;

QY 4 QNKPPSKPNDFHFEVFNVPSCISNNPTCWAIC-----KRIPNKKP 46

Db 152 ESNPPENHQNDFHFEVFNVPSCSTCEGNPACSPICQIGLERAPSR 198
 : : : : : |||| | | : : : ||| : : : |

RESULT 13
 VGLG_BRSVS
 ID VGLG_BRSVS STANDARD; PRT; 257 AA.
 AC O10686;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).
 GN G.

OS Bovine respiratory syncytial virus (strain Snook) (BRS).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
 OX NCBI_TaxID=82824;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=97288324; PubMed=9143302;
 RA Furze J., Roberts S., Wertz G., Taylor G.;
 RT "Antigenically distinct G glycoproteins of BRSV strains share a high
 RT degree of genetic homogeneity.";
 RL Virology 231:48-58(1997).

CC -!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
 CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
 CC HEMAGGLUTININATING ACTIVITIES.

CC -!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
 CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.

CC -!- SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B
 CC HRS VIRUS.

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 CC or send an email to license@isb-sib.ch).

DR EMBL; Y08719; CAA69969.1; -.
 DR HSP; P22261; IBRV.
 DR InterPro; IPR000925; -.
 DR Pfam; PF00802; Glycoprotein_G; 1.

KW Transmembrane; Glycoprotein.
 FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 38 66 POTENTIAL.
 FT DOMAIN 67 257 EXTRACELLULAR (POTENTIAL).
 FT DISULFID 173 186 BY SIMILARITY.
 FT CARBOHYD 176 182 BY SIMILARITY.
 FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 257 AA; 28362 MW; 09BDE6874421E79B CRC64;

Query Match 26.9%; Score 77.5; DB 1; Length 257;
 Best Local Similarity 30.8%; Pred. No. 0.03;
 Matches 16; Conservative 8; Mismatches 19; Indels 9; Gaps 2;

QY 6 KPPSKP-----NNDFH--FEVFNVPSCISNNPTCWAICKRIPNKKPKG 48
 ||| | : : : |||| | | : : : ||| : : : |

Db 145 KPPINPSSGIPENHQNDFHFEVFNVPSCSTCEGNLACLCLSIETRAPSR 196
 : : : : : |||| | | : : : ||| : : : |

RESULT 14
 VGLG_BRSVW
 ID VGLG_BRSVW STANDARD; PRT; 263 AA.
 AC O10687;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE GN MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).
 OS Bovine respiratory syncytial virus (strain Whb) (BRV).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
 OX NCBI_TaxID=82825;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97288324; PubMed=9143302;
 RA Furze J., Roberts S., Wertz G., Taylor G.;
 RT "Antigenically distinct G glycoproteins of BRV strains share a high
 degree of genetic homogeneity";
 RL Virology 231:48-58(1997).
 CC -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
 CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
 CC HEMAGGLUTININATING ACTIVITIES.
 CC -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
 CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
 CC -1- SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B
 CC HRS VIRUS.
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 CC -----
 DR EMBL; Y08717; CA69967.1; .
 DR HSSP; P22261; IBRV.
 DR InterPro; IPR000925; .
 DR Pfam; PF00802; Glycoprotein_G; 1.
 KW Transmembrane; Glycoprotein.
 FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 38 66 POTENTIAL.
 FT DOMAIN 67 263 EXTRACELLULAR (POTENTIAL).
 FT DISULFID 173 186 BY SIMILARITY.
 FT DISULFID 176 182 BY SIMILARITY.
 FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 263 AA; 29050 MW; 0D06AF7FCB46B858 CRC64;
 Query Match 26.9%; Score 77.5; DB 1; Length 263;
 Best Local Similarity 29.0%; Pred. No. 0.031;
 Matches 20; Conservative 5; Mismatches 19; Indels 25; Gaps 3;
 QY 6 KPSPKP-----NNDFH--FEVFNVPSCISNNPTCWAIC-----KR 40
 DB 145 KPPINPGSNPENQHDHNSQTLPHVFCSTCEGNPACSSLCQIGPERASSRAPITILKK 204
 QY 41 IPNKKPGKK 49
 DB 205 TPKPKTKK 213
 RESULT 15
 VGLG_ORSVW
 ID VGLG_ORSVW STANDARD; PRT; 263 AA.
 AC Q86695;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).
 GN G.
 OS Bovine respiratory syncytial virus (strain WSU 83-1578) (ORSV).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
 OX NCBI_TaxID=79699;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=94103788; PubMed=8277288;
 RA Mallipeddi S.K., Samal S.K.;
 RT "Analysis of the ovine respiratory syncytial virus (RSV) G
 glycoprotein gene defines a subgroup of ungulate RSV";
 RL J. Gen. Virol. 74:2787-2791(1993).
 CC -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
 CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
 CC HEMAGGLUTININATING ACTIVITIES.
 CC -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
 CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
 CC -1- SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B
 CC HRS VIRUS.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; S67863; AAB29551.1; .
 DR EMBL; S67862; AAB29551.1; JOINED.
 DR HSSP; P22261; IBRV.
 DR InterPro; IPR000925; .
 DR Pfam; PF00802; Glycoprotein_G; 1.
 KW Transmembrane; Glycoprotein.
 FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 38 66 POTENTIAL.
 FT DOMAIN 67 263 EXTRACELLULAR (POTENTIAL).
 FT DISULFID 173 186 BY SIMILARITY.
 FT DISULFID 176 182 BY SIMILARITY.
 FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 263 AA; 29225 MW; 81A649C6047B3B71 CRC64;
 Query Match 26.9%; Score 77.5; DB 1; Length 263;
 Best Local Similarity 25.8%; Pred. No. 0.031;
 Matches 17; Conservative 10; Mismatches 18; Indels 21; Gaps 2;
 QY 4 QNKPSKPNNDF--HFEVFNVPSCISNNPTCWAIC-----KRP 42
 DB 151 QSNPSEIQQDYSDFOILPYVPCNICEGDSACLSLCQDRSESILDKALTTPKTPKPMF 210
 QY 43 NKKPGK 48
 DB 211 TKKPTK 216
 Search completed: May 21, 2001, 14:17:12
 Job time: 96 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 21, 2001, 14:15:22 ; Search time 19.45 Seconds
(without alignments)
295.280 Million cell updates/sec

Title: US-09-202-035-1

Perfect score: 288

Sequence: 1 KORQNKPSKPNDFHFVFN.....NNPTCWAICKRIPNKKPGKK 49

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL15.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp-organelle.*
9: sp-phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_unclassified.*
13: sp_vertebrate.*
14: sp_virus.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	288	100.0	293	14	Q9YVB3
2	285	99.0	278	14	Q9Q6U1 human respi
3	285	99.0	278	14	Q9Q6T7 human respi
4	285	99.0	278	14	Q9Q6T4 human respi
5	285	99.0	278	14	Q9Q6T3 human respi
6	285	99.0	278	14	Q9Q6T0 human respi
7	285	99.0	279	14	Q9Q6U0 human respi
8	285	99.0	279	14	Q9Q6T9 human respi
9	285	99.0	279	14	Q9Q6T8 human respi
10	285	99.0	279	14	Q9Q6T5 human respi
11	285	99.0	279	14	Q9Q6T2 human respi
12	285	99.0	279	14	Q9Q6S9 human respi
13	285	99.0	279	14	Q9Q6S7 human respi
14	285	99.0	279	14	Q9Q6S6 human respi
15	285	99.0	279	14	Q9Q6S0 human respi
16	285	99.0	279	14	Q9Q6R9 human respi
17	285	99.0	292	14	Q9YVB2 human respi
18	285	99.0	292	14	Q9YVB0 human respi
19	285	99.0	295	14	Q86356 respiratory

20	285	99.0	295	14	Q86359	Q86359 respiratory
21	285	99.0	295	14	Q86360	Q86360 respiratory
22	285	99.0	297	14	Q82057	Q82057 human respi
23	285	99.0	297	14	Q82058	Q82058 human respi
24	285	99.0	297	14	Q82066	Q82066 human respi
25	285	99.0	297	14	Q82067	Q82067 human respi
26	285	99.0	297	14	Q82071	Q82071 human respi
27	285	99.0	297	14	Q82074	Q82074 human respi
28	285	99.0	297	14	Q82078	Q82078 human respi
29	285	99.0	297	14	Q9YVB5	Q9YVB5 human respi
30	285	99.0	297	14	Q82065	Q82065 human respi
31	285	99.0	298	14	Q82068	Q82068 human respi
32	285	99.0	298	14	Q82073	Q82073 human respi
33	285	99.0	298	14	Q09634	Q09634 human respi
34	285	99.0	298	14	Q09719	Q09719 respiratory
35	285	99.0	298	14	Q01929	Q01929 human respi
36	280	97.2	279	14	Q9Q6S8	Q9Q6S8 human respi
37	280	97.2	293	14	Q9YVB1	Q9YVB1 human respi
38	280	97.2	296	14	Q86358	Q86358 respiratory
39	280	97.2	297	14	Q91944	Q91944 human respi
40	280	97.2	298	14	Q82056	Q82056 human respi
41	280	97.2	298	14	Q82060	Q82060 human respi
42	280	97.2	298	14	Q82061	Q82061 human respi
43	280	97.2	298	14	Q82062	Q82062 human respi
44	280	97.2	298	14	Q82075	Q82075 human respi
45	280	97.2	298	14	Q82076	Q82076 human respi

ALIGNMENTS

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RESULT 1
Q9YVB3
ID Q9YVB3 PRELIMINARY: PRT: 293 AA.
AC Q9YVB3;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE ATTACHMENT GLYCOPROTEIN G (FRAGMENT).
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WV6973;
RX MEDLINE=9022964; PubMed=9806017;
RA Sullender W.M., Mufson M.A., Prince G., Anderson L.J., Wertz G.W.;
RT "Antigenic and genetic diversity among the attachment proteins of
RT group A respiratory syncytial viruses that have caused repeat
RT infections in children."
RL J. Infect. Dis. 178:925-932(1998).
DR EMBL: AF065407; AAD02943.1; -
DR INTERPRO: IPR000255; -
DR INTERPRO: IPR002965; -
DR PFAM: PF00802; Glycoprotein_G; 1.
DR PRINTS: PR01217; PRICHEXTENS.
DR PROSITE: PS00012; PHOSPHOPANTHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 293 AA; 32125 MW; 17B5B43396A63CCF CRC64;

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Query Match 100.0%; Score 288; DB 14; Length 293;
Best Local Similarity 100.0%; Pred. NO. 4.5e-30;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQNKPSKPNDFHFVFNFCISCSNNPTCWAICKRIPNKKPGKK 49
|||||
Db 144 KORQNKPSKPNDFHFVFNFCISCSNNPTCWAICKRIPNKKPGKK 192

RESULT 2


```

GN Human respiratory syncytial virus.
OS Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=92011;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroup A and B respiratory syncytial viruses isolated over nine
RT consecutive epidemics.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF193308; AAF23731.1; -
DR INTERPRO; IPR000255; -
DR PFAM; PF00802; Glycoprotein_G; 1.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 279 AA; 30499 MW; 4E1CDF2F7E569E3A CRC64;

Query Match 99.0%; Score 285; DB 14; Length 279;
Best Local Similarity 98.0%; Pred. No. 1.le-29;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNDFHFEVFNVPSCSICSNPTCWAICKRIPNKKPGKK 49
DB 130 KORQKPPKNPNDFHFEVFNVPSCSICSNPTCWAICKRIPNKKPGKK 178

RESULT 10
QY06T5 ID QY06T5 PRELIMINARY; PRT; 279 AA.
AC QY06T5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE GLYCOPROTEIN (FRAGMENT).
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=92415;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroup A and B respiratory syncytial viruses isolated over nine
RT consecutive epidemics.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF193311; AAF23734.1; -
DR INTERPRO; IPR000255; -
DR INTERPRO; IPR000925; -
DR PFAM; PF00802; Glycoprotein_G; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 279 AA; 30442 MW; F33F5932FCE77E89 CRC64;

Query Match 99.0%; Score 285; DB 14; Length 279;
Best Local Similarity 98.0%; Pred. No. 1.le-29;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNDFHFEVFNVPSCSICSNPTCWAICKRIPNKKPGKK 49
DB 130 KORQKPPKNPNDFHFEVFNVPSCSICSNPTCWAICKRIPNKKPGKK 178

RESULT 11

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QY06T2 ID QY06T2 PRELIMINARY; PRT; 279 AA.
AC QY06T2;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE GLYCOPROTEIN (FRAGMENT).
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=93057;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroup A and B respiratory syncytial viruses isolated over nine
RT consecutive epidemics.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF193314; AAF23737.1; -
DR INTERPRO; IPR000255; -
DR INTERPRO; IPR000925; -
DR PFAM; PF00802; Glycoprotein_G; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 279 AA; 30547 MW; 86DFD42DC8A8F500 CRC64;

Query Match 99.0%; Score 285; DB 14; Length 279;
Best Local Similarity 98.0%; Pred. No. 1.le-29;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNDFHFEVFNVPSCSICSNPTCWAICKRIPNKKPGKK 49
DB 130 KORQKPPKNPNDFHFEVFNVPSCSICSNPTCWAICKRIPNKKPGKK 178

RESULT 12
QY06S9 ID QY06S9 PRELIMINARY; PRT; 279 AA.
AC QY06S9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE GLYCOPROTEIN (FRAGMENT).
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95026;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroup A and B respiratory syncytial viruses isolated over nine
RT consecutive epidemics.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF193317; AAF23740.1; -
DR INTERPRO; IPR000255; -
DR INTERPRO; IPR000925; -
DR PFAM; PF00802; Glycoprotein_G; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 279 AA; 30529 MW; AEC4D787983D472D CRC64;

Query Match 99.0%; Score 285; DB 14; Length 279;

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Best Local Similarity 98.0%; Pred. No. 1.1e-29;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KORQNKPPKPNDFHFEVFNVPSCISCSNNPTCWAICKRIPNKKPGKK 49
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 130 KORQNKPPKPNDFHFEVFNVPSCISCSNNPTCWAICKRIPNKKPGKK 178

RESULT 13
Q906S7
ID Q906S7 PRELIMINARY; PRT; 279 AA.
AC Q906S7;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE GLYCOPROTEIN (FRAGMENT).
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID-11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-95118;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroup A and B respiratory syncytial viruses isolated over nine
RT consecutive epidemics";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF193319; AAF23742.1; -
DR INTERPRO; IPR000255; -
DR INTERPRO; IPR000925; -
DR INTERPRO; IPR002965; -
DR PFAM; PF00802; Glycoprotein_G; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 279 AA; 30501 MW; AED64E0C9AA4CC2D CRC64;

Query Match 99.0%; Score 285; DB 14; Length 279;
Best Local Similarity 98.0%; Pred. No. 1.1e-29;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KORQNKPPKPNDFHFEVFNVPSCISCSNNPTCWAICKRIPNKKPGKK 49
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 130 KORQNKPPKPNDFHFEVFNVPSCISCSNNPTCWAICKRIPNKKPGKK 178

RESULT 14
Q906S6
ID Q906S6 PRELIMINARY; PRT; 279 AA.
AC Q906S6;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE GLYCOPROTEIN (FRAGMENT).
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID-11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-95107;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroup A and B respiratory syncytial viruses isolated over nine
RT consecutive epidemics";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF193320; AAF23743.1; -
DR INTERPRO; IPR000255; -
DR INTERPRO; IPR000925; -

DR INTERPRO; IPR002965; -
DR PFAM; PF00802; Glycoprotein_G; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 279 AA; 30445 MW; F4D236EBE9E694A9E CRC64;

Query Match 99.0%; Score 285; DB 14; Length 279;
Best Local Similarity 98.0%; Pred. No. 1.1e-29;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KORQNKPPKPNDFHFEVFNVPSCISCSNNPTCWAICKRIPNKKPGKK 49
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Db 130 KORQNKPPKPNDFHFEVFNVPSCISCSNNPTCWAICKRIPNKKPGKK 178

RESULT 15
Q906S0
ID Q906S0 PRELIMINARY; PRT; 279 AA.
AC Q906S0;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE GLYCOPROTEIN (FRAGMENT).
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID-11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-98523;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroup A and B respiratory syncytial viruses isolated over nine
RT consecutive epidemics";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF193326; AAF23749.1; -
DR INTERPRO; IPR000255; -
DR INTERPRO; IPR000925; -
DR INTERPRO; IPR002965; -
DR PFAM; PF00802; Glycoprotein_G; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 279 AA; 30467 MW; EAF3C99707A9DB47 CRC64;

Query Match 99.0%; Score 285; DB 14; Length 279;
Best Local Similarity 98.0%; Pred. No. 1.1e-29;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KORQNKPPKPNDFHFEVFNVPSCISCSNNPTCWAICKRIPNKKPGKK 49
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 130 KORQNKPPKPNDFHFEVFNVPSCISCSNNPTCWAICKRIPNKKPGKK 178

Search completed: May 21, 2001, 14:17:00
Job time: 98 sec

